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Access DB# 68313

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
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 jan.delaval@uspto.gov

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	Type of Search	Vendors and cost where applicable
Searcher: <u>[Signature]</u>	NA Sequence (#) _____	STN <input checked="" type="checkbox"/>
Searcher Phone #: <u>4458</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>6/10/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>6/10/02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>60</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>150</u>	Other _____	Other (specify) _____

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Mon Jun 10 06:42:48 2002

: Entered [jdelaval 10-Jun-02 5:57]
09-251073
e11dvl

09-251073.pep

Page 1

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 14.16 Seconds
(without alignments)
33.930 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 e11dv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
No matches found				

Search completed: June 10, 2002, 06:28:47
Job time: 36 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:29:26 ; Search time 11.79 seconds
(without alignments)
16.421 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 e1dv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Query Match	Length DB ID	Description

No matches found			

Search completed: June 10, 2002, 06:33:29
Job time: 243 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 24.93 Seconds
(without alignments)
34.696 Million cell updates/sec

Title: 09-251073

Perfect score: 23

Sequence: 1 eildv 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 100 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rvirus:*
16: SP bacteriaph:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
No matches found							

Search completed: June 10, 2002, 06:30:53
Job time: 162 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 15.32 Seconds
(without alignments)
25.031 Million cell updates/sec

Title: 09-251073

Perfect score: 23

Sequence: 1 elldv 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 233302 seqs, 76696041 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/RCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
---------------	-------	----------------	--------	----	-------------

No matches found

Search completed: June 10, 2002, 06:31:29
Job time: 198 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 24.35 Seconds
(without alignments)
22,808 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eldv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq_032802:*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	5	17	AAK95719
2	23	100.0	5	18	AAW25192
3	23	100.0	5	19	AAW46318
4	23	100.0	5	20	AAV03855
5	23	100.0	5	21	AAV80488
6	23	100.0	5	21	AAV77442
7	23	100.0	5	21	AAV69619
8	23	100.0	5	22	AAW73465
9	23	100.0	5	22	AAW91966
10	23	100.0	5	22	AAW50876
11	23	100.0	5	22	AAW59135

ALIGNMENTS

RESULT 1

AAK95719

ID AAK95719 standard; peptide; 5 AA.

XX

AC AAK95719;

XX

DT 04-DEC-1996 (first entry)

XX

DE Alpha-4Beta-1 integrin binding inhibitory peptide 16.

XX

KM VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;

KW inhibitor; binding; white blood cell; migration; capillary wall;

KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;

KW CSI; CSI; HI; LDV; active site.

XX

XX Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5 /note="Val-NH2"

FT

XX US5510332-A.

XX

PD 23-APR-1996.

XX

PF 07-JUL-1994; 94US-0271830.

XX

PR 07-JUL-1994; 94US-0271830.

XX

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

PI Beck PJ, Kogan TP, Ren K, Vanderslice P;

PI WPI; 1996-221274/22.

XX

DR

XX

PT New peptide(s) based on the LDV domain of fibronectin - used for

PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,

PT fibronectin or Invasin

XX

PS Disclosure: Column 21-22; 35pp; English.

XX

CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the

CC surface of endothelial cells that line the interior wall of capillaries.

CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or

CC VLA-4 for very late antigen-4), a heterodimeric protein present on the

CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows

CC white blood cells to adhere to the capillary wall in areas where the

CC tissue surrounding the capillary has been infected or damaged. Sometimes

CC this white blood cell migration can become uncontrolled, with white

CC blood cells flooding to the scene, causing widespread tissue damage.

CC Cpts. capable of blocking this process may be beneficial as therapeutic

CC agents. IA4B1 also recognises the extracellular matrix glycoprotein

CC fibronectin. Three distinct IA4B1-binding sites have been identified

CC within fibronectin. One site is found in the Heparin region and is

CC expressed in all isoforms; two others (CSI and CSI) are present in the

CC alternatively spliced type III connecting segments. CSI has the higher

CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active

CC site. Peptides AAK95704-805 are modeled after a portion of the CSI

CC peptide that include the LDV domain presented in such a way by its novel

CC flanking sequence to produce a potent inhibitor of IA4B1 binding.

XX

SQ

Sequence 5 AA:

Query Match 100.0%; Score 23; DB 17; Length 5;

Best Local Similarity 100.0%; Prod. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
| | | | |
Db 1 eildv 5

RESULT 2

AAW25192 standard; peptide; 5 AA.
AAW25192:

05-JAN-1998 (first entry)

LDV-peptide capable of binding cell adhesion molecules.

LDV; leucine; aspartic acid; valine; cell adhesion molecule;
binding; bladder irrigation; tumour removal; endoscopic operation;
transurethral resection; cancer; neoplasia.

Synthetic.

DEL9529909-A1.

20-FEB-1997.

15-AUG-1995; 95DE-1029909.

15-AUG-1995; 95DE-1029909.

(FREP) FRESENTIUS AG.

Boehle A;

WPI; 1997-133793/13.

Endoscopic irrigation solns. - contg. peptide(s) that bind to cell

adhesion molecules

Claim 6; Page 8; 8pp; German.

AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
The peptides are capable of binding to cell adhesion molecules and
are used in aqueous irrigation solutions for use during and after
endoscopic operations. Preferred irrigation solutions are
electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
GRRP, VTR, YIGSR, KOAGDV and/or REDV (given in one letter amino acid
code). The solutions are especially used for irrigating the bladder
during and after tumour removal by transurethral resection. The
peptides protect against recurrence of tumours.

Sequence 5 AA;

Query Match 100.0%; Score 23; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
| | | | |
Db 1 eildv 5

RESULT 3

AAW46318 standard; protein; 5 AA.

AAW46318:

08-MAY-1998 (first entry)

Peptide recognised by integrin alpha4beta1.

Fibrinogen; integrin; alpha-IIb-beta3; cell surface receptor;
penton base protein; coat proteins; adenovirus; binding site;
cellular adhesion; extracellular matrix molecule; binding domain;
cell surface binding site; bispecific molecule; gene therapy.

Unidentified.

US5712136-A.

27-JAN-1998.

17-APR-1996; 96US-0634060.

08-SEP-1994; 94US-0303162.

(GENV-) GENVEC INC.

Brough DE, Bruder JT, Kovesdi I, McVey DL, Roelvink PW;
Wickham TJ;

WPI; 1998-119984/11.

Methods for introducing adenovirus into cells - used for genetic
engineering and gene therapy

Claim 27; Column 2; 56pp; English.

The present sequence is a linear stretch of amino acids (present in
fibronectin) recognised by the integrin alpha4beta1. Integrins are
cell surface receptors. The penton base protein (one of the coat
proteins) of adenoviruses binds to integrins. The integrins not only
provide a binding site for the adenoviral penton base protein, but also
mediate cellular adhesion to the extracellular matrix molecules. The
specification describes a method of introducing an adenovirus into
a cell in vitro having a particular cell surface binding site. The
adenovirus is contacted with a bispecific molecule comprising a component
that selectively binds a binding domain of the penton base protein of the
adenovirus and a second component that selectively binds the cell surface
binding site. A complex of the adenovirus and the bispecific molecule is
formed, and the cell is contacted with it to allow entry of the
adenovirus into the cell. The methods can be used for research and the
vectors can be used for gene therapy.

Sequence 5 AA;

Query Match 100.0%; Score 23; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
| | | | |
Db 1 eildv 5

RESULT 4

AAV03855 standard; peptide; 5 AA.

AAV03855:

16-JUN-1999 (first entry)

Integrin ligand dissociator (ILD) peptide.

Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke;
fibrinogen; glycoprotein IIb-IIIa; angina; myocardial infarction; bone;
osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
organ transplant rejection; arthritis; ILD.

Synthetic.

PN 4 WO9911280-A1.
XX
PD 11-MAR-1999.
XX
XX 03-SEP-1998; 98WO-US18305.
PF
XX 03-SEP-1997; 97US-0057463.
PR
XX (BURN-) BURNHAM INST.
PA
XX Hu DD, Smith JW;
PI WPI: 1999-243586/20.
DR
XX Disaggregating a ligand: integrin receptor complex
XX
PS Disaggregating a ligand: integrin receptor complex
XX
XX Disaggregating a ligand: integrin receptor complex
XX
XX The invention relates to integrin ligand dissociators. Disaggregation of
CC an existing platelet thrombus in a blood vessel is due to dissociation of
CC fibrinogen from glycoprotein IIB-IIIa. This dissociation is caused by the
CC binding of an integrin-ligand dissociator at ligand binding site I of
CC glycoprotein IIB-IIIa. The invention provides a method of disaggregating
CC an existing platelet thrombus in a blood vessel, where the platelet
CC thrombus may form an occlusion of a blood vessel, in a subject comprises
CC administering a compound which dissociates fibrinogen bound to a first
CC site on platelet glycoprotein IIB-IIIa, by binding to a second
CC interacting site on platelet glycoprotein IIB-IIIa, disaggregating the
CC platelet thrombus. The method is used to treat humans with unstable
CC angina, stroke and/or acute myocardial infarction. The methods can be
CC used to enact de-adhesion of osteoclasts from the bone surface to halt
CC bone loss in a patient with osteoporosis. The methods can also be used
CC for the de-adhesion of angiogenic endothelial cells in a patient with a
CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
CC retinopathy, psoriasis. The methods can also be used to treat tumours,
CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
CC bowel disease, or organ transplant rejection, and asthma. The methods can
CC be used for the dissolution of pre-formed platelet aggregates, which is a
CC departure from the current strategy of treatment prior to formation of
CC vascular occlusions. The present sequence represents an integrin ligand
CC dissociator (ILD) that can be used in the method of the invention.
XX
SO Sequence 5 AA:

Query Match 100.0%; Score 23; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
DB 1 elldv 5

RESULT 5
ID AAY80488 standard; peptide; 5 AA.
XX
AC AAY80488;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cell adhesion peptide #23.
XX
XX Bone regenerative; osteopathic; osseous tissue; reconstitution;
KM scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoclast; osteoclast; bone defect; fracture.
XX
OS Synthetic.
XX
XX WO200004941-A1.
PN
XX
PD 03-FEB-2000.

XX
XX 22-JUL-1999; 99WO-US16800.
PF
XX
XX 24-JUL-1998; 98US-0122348.
PR
XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX
XX Budny JA;
PI
XX WPI: 2000-195084/17.
DR
XX
XX System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption
XX
PS Claim 14; Page 32; 44pp; English.
XX
XX The invention relates to a novel system for reconstruction of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes
CC bone formation and a component that decreases bone resorption (II).
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (I) is preferably selected from: selectin or selection binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC metalloproteinase inhibitors. The peptides AAY80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (I) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.
XX
SO Sequence 5 AA:

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
DB 1 elldv 5

RESULT 6
ID AAY77442 standard; peptide; 5 AA.
XX
AC AAY77442;
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CSI-derived peptide #33.
XX
XX Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KM CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Mammalia.
XX
XX WO200002903-A1.
PN
XX
XX 20-JAN-2000.
PD
XX 15-DEC-1998; 98WO-US26605.
PF
XX
XX 10-JUL-1998; 98US-0113689.
PR
XX
XX (CYTE-) CYTEL CORP.
PA
XX

PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX WPI; 2000-182213/16.
DR
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders
XX
XX
PS Disclosure; Fig 2; 243pp; English.
CC The invention relates to peptidomimetic compounds (AAV77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAV77411-Y77414
CC and AAV77433-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAV77410).
XX
SQ Sequence 5 AA:
OY 1 eildv 5
DB 1 eildv 5
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 7
AA69619
ID AAV69619 standard; peptide; 5 AA.
XX
AC AAV69619;
XX
DT 19-APR-2000 (first entry)
XX
DE VLA-4 inhibitor peptide #2.
XX
XX LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
KW CD49/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative;
KW arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder;
KW autoimmune disorder; respiratory disorder; LDV motif.
XX
OS Synthetic.
XX
PN WO200000477-A1.
XX
PD 06-JAN-2000.
XX
XX 31-MAY-1999; 99WO-IB00973.
PF
XX 30-JUN-1998; 98US-0091180.
PR
XX
PA (PFIZ) PFIZ RR PROD INC.

XX
PI Duplantier AJ, Milici AJ, Chupak LS;
XX WPI; 2000-126762/11.
DR
XX
XX Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives
PT
XX
XX Disclosure; Page 2; 120pp; English.
CC The invention relates to novel arylalkyl and arylureidoalkyl
CC azolylalkanoic acid derivatives and related compounds (I), and their
CC salts and prodrugs. These are are integrin inhibitors, specifically of
CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49/CD29),
CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
CC inducible cell surface protein VCAM-1 (vascular cell adhesion
CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
CC and consequent or associated pathogenic processes mediated by VLA-4, and
CC may therefore be useful in the treatment and prevention of inflammatory,
CC autoimmune, or respiratory disorders. These include asthma, arthritis,
CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
CC inflammatory bowel disease. Sequences AAV69618-Y69620 represent peptides
CC derived from the VLA-4-binding domain of the FN CS-1 region which
CC contain the LDV motif and are known to inhibit fibronectin-dependent
CC cell adhesion.
XX
SQ Sequence 5 AA:
OY 1 eildv 5
DB 1 eildv 5
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 8
AAB73465
ID AAB73465 standard; peptide; 5 AA.
XX
AC AAB73465;
XX
DT 02-JUL-2001 (first entry)
XX
DE Fibronectin VLA-4 binding domain-derived pentapeptide #1.
XX
XX Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
KW very late antigen; antibody; kidney disease; chronic renal failure;
KW end-stage renal disease; chronic diabetic nephropathy;
KW diabetic glomerulopathy; diabetic renal hypertrophy;
KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
KW nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
XX
OS Unidentified.
XX
PN WO200119396-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25140.
XX
PR 14-SEP-1999; 99US-0153826.
XX
XX (BIOJ) BIOGEN INC.
PA (UNIO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX
PI Allen A, Pusey C, Lobb R;
XX
DR WPI; 2001-273408/28.
XX

PT Treating a mammal in, or at a risk of developing, chronic renal
PT failure, involves administering at least one integrin antagonist to the
PT mammal
PS
XX
XX
PS Disclosure: Page 24; 62pp; English.
XX
XX The invention relates to a method for treating a mammal with,
CC or at risk of developing, chronic renal failure, involving the
CC administration of at least one integrin antagonist. The integrin
CC antagonists that may be used in the method include antagonists of
CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
CC containing integrins. In particular, the antagonists are antibodies
CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
CC The method of the invention may be used to treat chronic renal failure,
CC end-stage renal disease, chronic diabetic nephropathy, diabetic
CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
CC hyperplastic glomerulosclerosis, chronic glomerulonephritis, hereditary
CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
CC peptides derived from the VLA-4 binding domain (CS-1 region) of
CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
CC therefore be used in the method of the invention.
XX
XX Sequence 5 AA:
SQ

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
| | | | |
DB 1 elldv 5

RESULT 9

AAB91966
ID AAB91966 standard; Peptide; 5 AA.

XX
AC AAB91966;

XX
DT 22-JUN-2001 (first entry)

XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.

XX
KM Protection: endogenous therapeutic peptide; peptidase: conjugation;
KM blood component: modification; succinimide; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX
OS Homo sapiens.

OS
XX Synthetic.

XX
PN WO200069900-A2.

XX
PD 23-NOV-2000.

XX
PF 17-MAY-2000; 2000MO-US13576.

XX
PR 17-MAY-1999; 99US-0134406.

XX
PR 10-SEP-1999; 99US-0153406.

XX
PR 15-OCT-1999; 99US-0159783.

XX
PA (CONT-) CONJUCHEM INC.

XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX
DR WPI; 2001-112059/12.

XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT

XX
PS Disclosure: Page 569; 733pp; English.
XX
XX

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 5 AA:

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
| | | | |
DB 1 elldv 5

RESULT 10

AAB50876
ID AAB50876 standard; peptide; 5 AA.

XX
AC AAB50876;

XX
DT 19-MAR-2001 (first entry)

XX
DE Integrin recognition peptide sequence #3.

XX
KM Integrin: transmembrane protein; alpha4 integrin inhibitor;

XX
KM paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
KM multiple sclerosis; asthma; atherosclerosis; wound healing.

XX
OS Unidentified.

XX
PN WO200073342-A1.

XX
PD 07-DEC-2000.

XX
PF 01-JUN-2000; 2000MO-US15153.

XX
PR 01-JUN-1999; 99US-0323447.

XX
PA (SCRI) SCRIPPS RES INST.

XX
PI Ginsberg MH, Pfaff M, Liu S;

XX
DR WPI; 2001-070959/08.

XX
PT Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT heptad repeats

XX
PS Disclosure: Page 2; 37pp; English.

XX
XX

CC The present sequence is given in a specification relating to a
CC polypeptide comprising a series of heptad-repeats that mimic a
CC transmembrane domain, and a selected cytoplasmic domain attached to the

CC heptad repeats. At least a portion of the polypeptide is prepared
CC recombinantly or at least 1 heptad repeat in the series has a different
CC amino acid sequence to other heptad repeats in the series. The
CC polypeptide is useful in the construction of structural models which are
CC useful for evaluating structure and activity of a selected occupied and
CC clustered transmembrane protein having the selected cytoplasmic domain
CC and for identifying therapeutic compounds. It is also useful for
CC identifying agents as inhibitors of alpha4 integrin biological
CC responses by contacting the structural model with paxillin or a
CC paxillin related molecule in the presence and absence of a test agent
CC and determining binding of paxillin or paxillin related molecule to the
CC structural model. A decrease in binding in the presence of the test
CC agent indicates that the test agent is an inhibitor of alpha4 integrin
CC biological response. Inhibitors of the binding of paxillin to alpha4 are
CC useful in blocking immune responses in conditions such as inflammatory
CC bowel disease, arthritis, multiple sclerosis and asthma and in
CC inhibiting atherosclerosis and scarring during wound healing.

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
Db 1 eildv 5

RESULT 11

AAB59135 AAB59135 standard; peptide; 5 AA.

XX AAB59135;

XX 21-MAR-2001 (first entry)

DE Peptide #3 recognised by Integrin.

XX Heptad repeat; transmembrane domain; cytoplasmic; Integrin;

KW Inflammation; thrombosis; malignancy.

OS Synthetic.

PN WO200073341-A1.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000WO-US14656.

PR 27-MAY-1999; 99US-0320907.

PA (SCRI) SCRIPPS RES INST.

PI Ginsberg MH, Pfaff M;

DR WPI; 2001-041143/05.

PT Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT the repeats -

XX Disclosure; Page 2; 36pp; English.

XX The present invention relates to a peptide with a series of
CC heptad-repeats that mimic a transmembrane domain and a selected
CC cytoplasmic domain attached to the heptad repeats. The invention
CC is useful for evaluating structure and activity of a selected
CC occupied and clustered transmembrane protein with the selected
CC cytoplasmic domain and for identifying therapeutic compounds. It
CC is also useful for identifying a cytoplasmic domain binding partner.

CC It is may be used to study protein interactions with transmembrane
CC proteins such as integrin, which can be used to treat conditions in
CC which over activity of integrins is involved, such as inflammation,
CC thrombosis and malignancy.

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
Db 1 eildv 5

Search completed: June 10, 2002, 06:30:08
Job time: 117 sec

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: June 10, 2002, 06:17:45 ; Search time 14.7 seconds
(without alignments)
32.683 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	50	2	B86576 hypothetical prote
2	23	100.0	50	2	C72047 hypothetical prote
3	23	100.0	107	2	S13787 conserved hypotet
4	23	100.0	119	1	A69441 conserved hypotet
5	23	100.0	119	2	F84272 hypothetical prote
6	23	100.0	143	2	C44259 kinasin heavy chain
7	23	100.0	146	2	E90645 probable PTS enzym
8	23	100.0	146	2	E85496 hypothetical prote
9	23	100.0	147	2	F70814 probable exported
10	23	100.0	147	2	AG0772 transcription elon
11	23	100.0	156	2	G82906 phosphoribosylamin
12	23	100.0	169	2	AH0568 stellate protein -
13	23	100.0	172	2	S24357 shikimate kinase (
14	23	100.0	172	2	AF0390 hypothetical prote
15	23	100.0	174	2	S24398 uncharacterized co
16	23	100.0	174	2	F97114 hypothetical prote
17	23	100.0	177	2	A64431 conserved hypotet
18	23	100.0	180	2	G95148 conserved hypotet
19	23	100.0	180	2	E98016 hypothetical prote
20	23	100.0	200	2	T48130 modulation protein
21	23	100.0	217	1	ZZZRM4 nodB chitooligosac
22	23	100.0	217	1	ZZZRB4 conserved hypotet
23	23	100.0	222	2	C72400 hypothetical prote
24	23	100.0	231	2	B98297 conserved hypotet
25	23	100.0	231	2	AE2966 conserved hypotet
26	23	100.0	242	2	A69026 hypothetical prote
27	23	100.0	250	2	B91020 hypothetical prote
28	23	100.0	250	2	D85864 hypothetical prote
29	23	100.0	250	2	D85864

30	23	100.0	253	2	H70188 conserved hypotet
31	23	100.0	256	2	T32649 hypothetical prote
32	23	100.0	261	2	C55581 nssd protein - Kle
33	23	100.0	266	2	A95300 Nitrate transport
34	23	100.0	267	2	H90388 erythrocyte band 7
35	23	100.0	267	2	C64995 hypothetical prote
36	23	100.0	271	2	C66907 regulator of purin
37	23	100.0	286	2	S01402 H+-transporting AT
38	23	100.0	289	2	E97820 3-demethylubiquino
39	23	100.0	290	2	T21185 hypothetical prote
40	23	100.0	307	2	G81905 probable sulfate a
41	23	100.0	307	2	B81111 sulfate adenylyltr
42	23	100.0	307	2	S20383 phytoene synthase
43	23	100.0	312	2	T41157 probable 60s acid
44	23	100.0	320	2	S73413 transcription anti
45	23	100.0	321	2	A95182 hypothetical prote

ALIGNMENTS

RESULT 1

B86576
hypothetical protein CPJ0685 [Imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: B86576
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishl, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: B86576
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <STO>
A:CROSS-references: GB:BA000008; NID:98979057; PIDN:BA98892.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0685

Query Match 100.0% Score 23; DB 2; Length 50;
Best Local Similarity 100.0% Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 eildv 5
DB 7 EILDV 11

RESULT 2

C72047
hypothetical protein - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: C72047
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: C72047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <ARN>
A:CROSS-references: GB:AE001651; GB:AE001363; NID:94376985; PIDN:AD018824.1; PID:9437
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: CPN0685

Query Match 100.0% Score 23; DB 2; Length 50;
Best Local Similarity 100.0% Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
Db 7 EILDV 11

RESULT 3
S13787

conserved hypothetical protein yaak - *Bacillus subtilis*

C:Species: *Bacillus subtilis*

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C:Accession: S13787; S66050; C69737

R:Alonso, J.C.; Shitahige, K.; Ogasawara, N.

Nucleic Acids Res. 18, 6771-6777, 1990

A:Title: Molecular cloning, genetic characterization and DNA sequence analysis of the re

A:Reference number: S13786; MUID:91088245

A:Accession: S13787

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <ALO>

A:Cross-references: EMBL:X17014; NID:9453238; PIDN:CAA34878.1; PID:940073

R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.

DNA Res. 1, 1-14, 1994

A:Title: Systematic sequencing of the 180 kilobase region of the *Bacillus subtilis* chrom

A:Reference number: S63967; MUID:96051385

A:Accession: S66050

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <OGA>

A:Cross-references: EMBL:D26185; NID:9467326; PIDN:BA05256.1; PID:9467410

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laidinols,

A:Authors: Lauder, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadale, Y.; Saito, T.; Scanlon,

A:Authors: Schleith, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togonni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wippl, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A:Reference number: A69580; MUID:98044033

A:Accession: C69737

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-107 <KUN>

A:Cross-references: GB:299104; GB:AL009126; NID:92632267; PIDN:CAB1196.1; PID:92632287

A:Experimental source: strain 168

C:Genetics:

A:Gene: yaak

C:Superfamily: *Escherichia coli* ybaB protein

Query Match 100.0%; Score 23; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
Db 52 EILDV 56

RESULT 4
A69441

conserved hypothetical protein AFI530 - *Archaeoglobus fulgidus*

C:Species: *Archaeoglobus fulgidus*

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: A69441

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attleach, P.; Kalne, B.P.; Sykes,

Smith, H.O.; Weese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343

A:Accession: A69441

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-119 <KLE>

A:Cross-references: GB:AE000997; GB:AE000782; NID:92689320; PIDN:AA89718.1; PID:9264

C:Superfamily: conserved hypothetical protein M0039

Query Match 100.0%; Score 23; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
Db 109 EILDV 113

RESULT 5
F84272

hypothetical protein Vng1169c [imported] - *Halobacterium* sp. NRC-1

C:Species: *Halobacterium* sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: F84272

R:Ng, W.V.; Kennedy, S.P.; Mahalras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky

C.; Lettner, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Ja

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.

A:Title: Genome sequence of *Halobacterium* species NRC-1.

A:Reference number: A84160; MUID:20504483

A:Accession: F84272

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-119 <STO>

A:Cross-references: GB:AE004437; NID:910580704; PIDN:ANG19546.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1169C

C:Superfamily: conserved hypothetical protein M0039

Query Match 100.0%; Score 23; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
Db 110 EILDV 114

RESULT 6
C44259

kinesin heavy chain homolog Kifs - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998

C:Accession: C44259

R:Alzawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.

J. Cell Biol. 119, 1287-1296, 1992

A:Title: Kinesin family in murine central nervous system.

A:Reference number: A44259; MUID:93077686

A:Accession: C44259

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-143 <AI2>

A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBI:118906)

C:Superfamily: kinesin heavy chain; kinesin motor domain homology

F:1-143/Domain: kinesin motor domain homology (fragment) <KNOT>

Query Match 100.0%; Score 23; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 elldv 5
|||||
Db 91 EILDV 95

RESULT 7
E90645
Probable PHS enzyme II B component [Imported] - Escherichia coli (strain O157:H7, subsp. C)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E90645
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gaswara, N.; Yasunaga, T.; Kunihara, S.; Shiba, T.; Hattori, M.; Shlnagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: E90645
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <NAV>
A:Cross-references: GB:BA000007; PIDN:BA833556.1; PID:q13359589; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC50133

Query Match 100.0%; Score 23; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 elldv 5
|||||
Db 15 EILDV 19

RESULT 8
E85496
Probable PHS enzyme II B component [Imported] - Escherichia coli (strain O157:H7, subsp. C)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85496
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca, N.
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85496
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <STO>
A:Cross-references: GB:AE005174; NID:q12512844; PIDN:AAG54433.1; GSPDB:GN00145; UWGP:201
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yadI

Query Match 100.0%; Score 23; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 elldv 5
|||||
Db 15 EILDV 19

RESULT 9

E70814
Hypothetical protein RV0854 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70814

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Genies, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: F70814

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-147 <COI>

A:Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAI17660.1; PID:q291
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV0854

C:Superfamily: Streptomyces coelicolor hypothetical protein SC6610.02c

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 elldv 5
|||||
Db 17 EILDV 21

RESULT 10
AG0772
Probable exported protein STY2351 [Imported] - Salmonella enterica subsp. enterica se
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0772
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AG0772
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <PAR>
A:Cross-references: GB:AL513382; PIDN:CADD2501.1; PID:q16503365; GSPDB:GN00176
C:Genetics:
A:Gene: STY2351

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 elldv 5
|||||
Db 98 EILDV 102

RESULT 11
G82906
Transcription elongation factor UUG304 [Imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: G82906
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum. Alternate views of a

A:Reference number: A82870
A:Accession: G82906
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-156 <GLA>
A:Cross-references: GB:AE002128; GB:AF222894; MID:g6899279; PIDN:AAF30713.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: greA; U0304
A:Gene: greA; U0304
A:Gene: greA; U0304
C:Superfamily: transcription elongation factor greB
C:Keywords: transcription factor

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 156;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
DB 20 EILDV 24

RESULT 12
AH0568
Phosphoribosylaminoimidazole carboxylase catalytic chain [imported] - Salmonella enteric
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH0568
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Th, T.; Connelton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AH0568
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05018.1; PID:g16501801; GSPDB:GN00176
C:Genetics:
A:Gene: STY0582
C:Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain: phosphoribosyla

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 169;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
DB 31 EILDV 35

RESULT 13
S24397
stellate protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C:Accession: S24397; S08120
R:Livak, K.J.
Genetics 124, 303-316, 1990
A:Title: Detailed structure of the Drosophila melanogaster stellate genes and their tran
A:Reference number: S24397; MUID:90169476
A:Accession: S24397
A:Molecule type: DNA
A:Residues: 1-172 <LIV>
A:Cross-references: EMBL:X15899; MID:g8660; PIDN:CAA33906.1; PID:g295755
C:Genetics:
A:Gene: stellate
A:Cross-references: FlyBase:FBgn0003523

A:introns: 4/2; 171/2

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 172;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
DB 46 EILDV 50

RESULT 14
S24398
stellate protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S24398
R:Livak, K.J.
Genetics 124, 303-316, 1990
A:Title: Detailed structure of the Drosophila melanogaster stellate genes and their t
A:Reference number: S24397; MUID:90169476
A:Accession: S24398
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <LIV>

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 172;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
DB 46 EILDV 50

RESULT 15
AF0390
shikimate kinase (EC 2.7.1.71) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 11-Jan-2002
C:Accession: AF0390
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
ll, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.; Whitehead, S.; Barrcl
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0390
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-174 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92450.1; PID:g15981151; GSPDB:GN00175
C:Genetics:
A:Gene: aroL
C:Superfamily: shikimate kinase: shikimate kinase homology
C:Keywords: phosphotransferase

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 174;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
DB 131 EILDV 135

Search completed: June 10, 2002, 06:23:16
Job time: 331 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:20:35 ; Search time 11.71 Seconds

(without alignments)
16.533 Million cell updates/sec

Title: 09-251073

Perfect score: 23

Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	107	1	YAAK_BACSU
2	23	100.0	121	1	PAND_MOLSU
3	23	100.0	156	1	GREU_UREPA
4	23	100.0	172	1	STEL_DROME
5	23	100.0	177	1	YASU_METUA
6	23	100.0	198	1	IFR2_ARATH
7	23	100.0	217	1	NODB_RHIME
8	23	100.0	229	1	ACHP_LYMST
9	23	100.0	259	1	DBA_MOUSE
10	23	100.0	262	1	NASD_KLEPN
11	23	100.0	267	1	YFAU_ECOLI
12	23	100.0	271	1	PURR_LACUA
13	23	100.0	286	1	ATPG_BACP3
14	23	100.0	287	1	ATPG_BACCA
15	23	100.0	287	1	ATPG_BACST
16	23	100.0	307	1	CRFB_SYNF7
17	23	100.0	320	1	Y054_MYCPN
18	23	100.0	332	1	SD22_SCHPO
19	23	100.0	338	1	DHAS_SHEEP
20	23	100.0	338	1	DHAS_SHEVI
21	23	100.0	342	1	LYC_CLOPE
22	23	100.0	344	1	FLIG_BORBU
23	23	100.0	351	1	DUB2_HUMAN
24	23	100.0	366	1	DP3B_ECOLI
25	23	100.0	366	1	DP3B_SALTY
26	23	100.0	380	1	P37_MYCPN
27	23	100.0	380	1	RRP2_ARCFU
28	23	100.0	380	1	YREP_BACSU
29	23	100.0	387	1	2A5E_MOUSE
30	23	100.0	394	1	CEGT_HUMAN
31	23	100.0	414	1	YAPA_ECOLI
32	23	100.0	414	1	YAPA_SALTY
33	23	100.0	435	1	2A5G_MOUSE

34	23	100.0	467	1	2A5E_HUMAN
35	23	100.0	472	1	YAB5_MOUSE
36	23	100.0	484	1	DCOR_NEUCR
37	23	100.0	486	1	2A5A_HUMAN
38	23	100.0	493	1	PVR5_DROME
39	23	100.0	497	1	2A5B_HUMAN
40	23	100.0	500	1	2A5B_RABIT
41	23	100.0	503	1	GLPK_PSETO
42	23	100.0	506	1	SYG_DEIRA
43	23	100.0	522	1	FINC_CANFA
44	23	100.0	522	1	FINC_HORSE
45	23	100.0	524	1	2A5G_HUMAN

ALIGNMENTS

```

RESULT 1
YAAK_BACSU STANDARD: PRT, 107 AA.
AC P24281;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yaak.
GN YAAK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088245; PubMed=2124672;
RA Alonso C., Shihahige K., Ogasawara N.;
RT "Molecular cloning, genetic characterization and DNA sequence
RT analysis of the recomb region of Bacillus subtilis."
RL Nucleic Acids Res. 18:6771-6777(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin."
RL DNA Res. 1:1-14(1994).
RN [3]
RP SIMILARITY: BELONGS TO THE UPF0133 FAMILY.
-----
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-----
CC EMBL: X17014; CAA34878.1;
CC EMBL: D26185; BAA05256.1;
CC EMBL: 299104; CAB11796.1;
CC PIR: S13787; S13787.
CC Subtilist: BG10084; YAAK.
CC InterPro: IPR003727; DUF149.
CC Pfam: PF02575; DUF149; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 107 AA; 11781 MW; DB3EBA3420F6A9E6 CRC64;
-----
Query Match 100.0%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. NO. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
DB 52 EILDV 56

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RESULT 2
PAND_MOLSU STANDARD: PRT: 121 AA.
AC 034246:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aspartate 1-decarboxylase precursor (EC 4.1.1.11) (Aspartate alpha-decarboxylase).
GN PAND.
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Molinella.
OX NCBI_TaxID=844;
RN [1]
RP SEQUENCE FROM N.A.
RA Gross R., Thels F., Kroegeer A.:
RT "Two membrane anchors of Wolinella succinogenes hydrogenase and their function in fumarate and polysulfide respiration."
RL Submitted (NCV-1997) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-aspartate -> beta-alanine + CO(2).
CC -1- COFACTOR: Pyruvoyl group (By similarity).
CC -1- PATHWAY: Pantothenate biosynthesis; second branch.
CC -1- SIMILARITY: BELONGS TO THE PAND FAMILY.
-----
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-----
DR EMBL: AJ003049; CAA05822.1; -.
DR HSSP: P31664; IAW8.
DR InterPro: IPR003190; Asp_decarbox.
DR Pfam: PF02261; Asp_decarbox; 1.
KW Pantothenate biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.
FT CHAIN 1 24 ASPARTATE 1-DECARBOXYLASE BETA CHAIN (BY SIMILARITY).
FT CHAIN 25 121 ASPARTATE 1-DECARBOXYLASE ALPHA CHAIN (BY SIMILARITY).
FT MOD_RES 25 25 CONVERTED TO A PYRUVOYL GROUP (BY SIMILARITY).
FT SEQUENCE 121 AA; 13601 MW; 41FB7B63B571F837 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
|1111
DB 45 EILDV 49

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RP SEQUENCE FROM N.A.
RC STRAIN-SEROVAR 3;
RX MEDLINE-20500219; PubMed-11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma urealyticum."
RL Nature 407:757-762(2000).
CC -1- FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION ELONGATION PAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY CLEAVAGE FACTORS SUCH AS GREB OR GREB ALLOWS THE RESUMPTION OF ELONGATION FROM THE NEW 3' TERMINUS. GREB RELEASES SEQUENCES OF 2 TO 3 NUCLEOTIDES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GREB/GREB FAMILY.
-----
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-----
DR EMBL: AE002128; AAF30713.1; -.
DR InterPro: IPR001437; GreA_Greb.
DR Pfam: PF01272; GreA_Greb; 1.
DR ProDom: PD004918; GreA_Greb; 1.
DR PROSITE: PS00829; GREAB.1; 1.
DR PROSITE: PS00830; GREAB.2; FALSE_NEG.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 7 24 COILED COIL (POTENTIAL).
FT DOMAIN 42 84 COILED COIL (POTENTIAL).
FT SEQUENCE 156 AA; 17767 MW; 86BEA8EC07C96461 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
|1111
DB 20 EILDV 24

```

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RESULT 4
STEL_DROME STANDARD: PRT: 172 AA.
AC P15021:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Stellate protein.
GN STE.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-OREGON-R; TISSUE-Testis;
RX MEDLINE=90169476; PubMed=1689686;
RA Liyak K.J.;
RT "Detailed structure of the Drosophila melanogaster stellate genes and their transcripts."
RL Genetics 124:303-316(1990).
CC -1- FUNCTION: RESPONSIBLE FOR THE APPEARANCE OF PROTEINACEOUS STAR-SHAPED CRYSTALS IN THE PRIMARY SPERMATOCYTES OF D.MELANOGASTER MALES LACKING A Y CHROMOSOME.
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE COPIES OF THE STELLATE GENE IN

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CC      FRUIT FLV.
CC      -1- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X15899; CAA33906.1; -
DR      PIR: S08120; S08120.
DR      PIR: S24397; S24397.
DR      FLYBase: FBgn0003523; Ste.
DR      InterPro: IPR000704; CAS_kinase_II.
DR      Pfam: PF01214; CK II beta; 1.
DR      PRINTS: PR00472; CASNKINASEII.
DR      PROSITE: PS01101; CK2_BETA; 1.
DR      TrEMBL: MultiGene family.
KW      testis; Multigene family.
SQ      SEQUENCE 172 AA; 19507 MW; C86304F591E76F8A CRC64;

Query Match          100.0%; Score 23; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 e1ldv 5
        |||||
DB      46 EILDV 50

RESULT 5
VASYO_METJA STANDARD; PRT: 177 AA.
ID VASYO_METJA
AC 058450:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1050.
GN MJ1050.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.W., Zhou L., Fleischmann R.D.,
RA Sult G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weissbrock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geophagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Cottenbach T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hann B.C.,
RA Gordon M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.W., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RT Science 273:1058-1073(1996).
RL -1- SIMILARITY: BELONGS TO THE UPF0101 FAMILY.
CC -----
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CC      -----
DR      EMBL: U67548; AAB99053.1; -
DR      TIGR: MJ1050; -
KW      Hypothetical protein; ATP-binding; Complete proteome.

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FT      NP_BIND 7 14 ATP (POTENTIAL).
SQ      SEQUENCE 177 AA; 20690 MW; F209572AA79CD2F9 CRC64;

Query Match          100.0%; Score 23; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 e1ldv 5
        |||||
DB      118 EILDV 122

RESULT 6
IFE2_ARATH STANDARD; PRT: 198 AA.
ID IFE2_ARATH
AC 004663; OGSAN8;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Eukaryotic translation initiation factor 4E (eIF-4E) (mRNA
DE cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(iso)4F p28
DE subunit) (eIF4E150 protein).
GN IFE2 OR AT5G35620 OR MJB4.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97378268; PubMed=9234949;
RA Wittmann S., Chateil H., Fortin M.G., Laliberté J.F.;
RA "Interaction of the viral protein genome linked of turnip mosaic
RT polyvirus with the translation eukaryotic initiation factor (iso)
RT 4E of Arabidopsis thaliana using the yeast two-hybrid system."
RL Virology 234:84-92(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Rodriguez C., Freire M.A., Robaglia C.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT DNA Res. 5:203-216(1998).
RT Physically assigned PI and YAC clones."
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT DNA Res. 5:203-216(1998).
CC -----
CC      -1- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE-CONTAINING
CC      MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN
CC      SYNTHESIS AND FACILITATES RIBOSOME BINDING BY INDICATING THE
CC      UNWINDING OF THE MRNA SECONDARY STRUCTURES (BY SIMILARITY).
CC      -1- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EIF4A
CC      (WHICH CAN CYCLE IN AND OUT OF THE COMPLEX). IN HIGHER PLANTS TWO
CC      ISOFORMS OF EIF4F HAVE BEEN IDENTIFIED, NAMED EIF4F AND
CC      EIF4F2. EIF4F HAS SUBUNITS P220 AND P28, WHEREAS EIF-(iso)4F
CC      HAS SUBUNITS P82 AND P26 (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U62044; AAB66906.1; ALT_INIT.
DR      EMBL: Y10547; CAA71579.1; -
DR      EMBL: AB013393; BAB09303.1; -

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DR HSSP; P07260; 1AP8.
DR InterPro; IPR001040; eIF_4E.
DR Pfam; PF01652; IF4E; 1.
DR ProDom; PD003697; eIF_4E; 1.
DR PROSITE; PS00813; IF4E; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding;
KW Multigene family.
SQ SEQUENCE 198 AA; 22514 MW; 71FEB309E073A9D2 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. NO. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 e1ldv 5
DB 175 EILDV 179

RESULT 7
NODE_RHIME STANDARD; PRT; 217 AA.
ID P02963; 052477;
AC 21-JUN-1986 (Rel. 01, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Chitooligosaccharide deacetylase (EC 3.5.1.-) (Modulation protein B).
GN NOB OR RA0474 OR SMA0868.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSyma (megaplasmid 1).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=85229955; PubMed=4006668;
RA Egelhof T.T., Fisher R.F., Jacobs T.W., Mulligan J.T., Long S.R.;
RT "Nucleotide sequence of Rhizobium meliloti 1021 modulation genes;"
RL DNA 4:241-248(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RX MEDLINE=85087953; PubMed=6336331;
RA Toerock I., Kondorosi E., Stepkowski T., Posfal J., Kondorosi A.;
RT "Nucleotide sequence of Rhizobium meliloti modulation genes.;"
RL Nucleic Acids Res. 12:9509-9524(1984).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=042B;
RA Yang X., Gao W.M., Yang S.S.;
RT "The complete sequence of S. meliloti 042B nodABC.;"
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barlow-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Hultzer L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSyma megaplasmid.;"
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC -1- FUNCTION: IS INVOLVED IN GENERATING A SMALL HEAT-STABLE COMPOUND
CC (NOD), AN ACYLATED OLIGOMER OF N-ACETYLGLUCOSAMINE, THAT
CC STIMULATES MITOSIS IN VARIOUS PLANT PROTOPLASTS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: TO OTHER POLYSACCHARIDE-DEACETYLASES.
CC -----
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CC -----
CC EMBL; M1268; AAA98361.1; -.
CC EMBL; X01649; CAA25809.1; -.
CC EMBL; AF038577; AAB95330.1; -.
CC EMBL; AF007237; AAK65132.1; -.
CC PIR; A03483; ZZZRBM.
CC PIR; A03484; ZZZRBM4.
DR InterPro; IPR002509; Polysac.deacet.
DR Pfam; PF01522; Polysac-deacet; 1.
KW Hydrolase; Modulation; Plasmid; Complete proteome.
FT VARIANT 10 10 V -> M (IN STRAIN 41).
FT VARIANT 59 59 A -> T (IN STRAIN 41).
FT VARIANT 116 116 H -> R (IN STRAIN 41).
FT VARIANT 195 198 ALSR -> GFPV (IN STRAIN 042B).
FT CONFLICT 108 118 ACPQAAVRRHR -> LVLRPSDYE (IN REF. 1).
SQ SEQUENCE 217 AA; 23671 MW; 01F82A0C75EA662D CRC64;

OY 1 e1ldv 5
DB 38 EILDV 42

Query Match 100.0%; Score 23; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. NO. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 e1ldv 5
DB 38 EILDV 42

RESULT 8
NODE_RHIME STANDARD; PRT; 229 AA.
ID ACHP_LYMST
AC P58154;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholine-binding protein precursor (ACh-binding protein) (AChBP).
OS Lymnaea stagnalis (great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 20-30, AND MASS SPECTROMETRY.
RC TISSUE=CNS;
RX MEDLINE=21256198; PubMed=11357121;
RA Smit A.B., Syed N.I., Schapp D., van Minnen J., Klumperman J.,
RA Kils K.S., Lodder H., van Der Schors R.C., van Elk R., Sorigedraeger B.,
RA Breijer K., Sixma T.K., Geraerts W.P.M.;
RT "A glia-derived acetylcholine-binding protein that modulates synaptic
RT transmission.;"
RL Nature 411:261-268(2001).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 20-229.
RX MEDLINE=21256199; PubMed=11357122;
RA Breijer K., van Dijk W.J., Klaassen R.V., Schuurmans M.,
RA van Der Oost J., Smit A.B., Sixma T.K.;
RT "Crystal structure of an ACh-binding protein reveals the
RT ligand-binding domain of nicotinic receptors.;"
RL Nature 411:269-276(2001).
CC -1- FUNCTION: BINDS TO ACETYLCHOLINE. MODULATES NEURONAL SYNAPTIC
CC TRANSMISSION.
CC -1- SUBUNIT: HOMOPENTAMER.
CC -1- SUBCELLULAR LOCATION: SECRETED. RELEASED IN AN ACETYLCHOLINE-
CC DEPENDENT MANNER IN THE SYNAPTIC CLEFT.
CC -1- TISSUE SPECIFICITY: EXPRESSED BY GLIAL CELLS.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- MASS SPECTROMETRY: MW=24720.4; METHOD=QTOF; RANGE=20-229.
CC -1- SIMILARITY: TO THE EXTRACELLULAR PORTION OF LIGAND-GATED IONIC
CC CHANNELS FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF364899; AAK64377.1; -.
DR PDB: 1I9B; 16-MAY-01.
KM Glycoprotein: Signal: 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 229 ACETYLCHOLINE-BINDING PROTEIN.
FT DISULFID 142 155
FT DISULFID 207 207
FT CARBOHYD 85 85 N-LINKED (GLCNAC... ) (PROBABLE).
SO SEQUENCE 229 AA; 26061 MW; B76A3A13E7EF8FCB CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 229;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
DB 191 EILDV 195

RESULT 9
DJB_A_MOUSE STANDARD; PRT; 259 AA.
ID DJB_A_MOUSE
AC 09OY15;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dnaj homolog subfamily B member 10 (mdj8).
GN DNABJ10.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21033480; PubMed=11147971;
RA Ohtsuka K., Hata M.;
RT "Mammalian HSP40/DNAJ homologs: cloning of novel cDNAs and a proposal
RT for their classification and nomenclature.";
RL Cell Stress Chaperones 5:98-112(2000).
CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
CC -----
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CC -----
DR EMBL: AB028858; BAA8306.1; -.
DR HSSP: P25685; 1JDU.
DR MGD: MGI:1928739; Dnajb10.
DR InterPro: IPR001623; Dnaj_N.
DR InterPro: IPR002950; Josephin.
DR InterPro: IPR003903; UIM.
DR Pfam: PF00226; Dnaj_1.
DR Pfam: PF02809; UIM_1.
DR SMART: SM00271; Dnaj_1.
DR SMART: SM00636; Dnaj_1; FALSE_NEG.
DR PROSITE: PS50076; Dnaj_2; 1.
KM Chaperone.
FT DOMAIN 3 71 J-DOMAIN.

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FT DOMAIN 133 140 POLY-SER.
SQ SEQUENCE 259 AA; 28601 MW; 81387B09AD9B09A CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 259;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
DB 6 EILDV 10

RESULT 10
NASD_KLEPN STANDARD; PRT; 262 AA.
ID NASD_KLEPN
AC P39459;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitrate transport protein nasd.
GN NASD.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSA1;
RX MEDLINE=94222832; PubMed=8169203;
RA Lin J.T., Goldman B.S., Stewart V.;
RT "The nasDEBCA operon for nitrate and nitrite assimilation in
RT Klebsiella pneumoniae MSA1.";
RL J. Bacteriol. 176:2551-2559(1994).
RN [2]
RP REVISIONS.
RC STRAIN=MSA1;
RA Stewart V.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-
CC DEPENDENT TRANSPORT SYSTEM FOR NITRATE. PROBABLY RESPONSIBLE FOR
CC ENERGY COUPLING TO THE TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC -----
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CC -----
DR EMBL: L27431; AAB86901.1; -.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran_1.
DR SMART: SM00382; AAA_1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1.
KW Transport; ATP-binding; Membrane; Nitrate assimilation.
FT NP_BIND 41 48
FT SEQUENCE 262 AA; 28996 MW; AD1B32490A2EA10 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 262;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
DB 222 EILDV 226

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RT "Sequence and over-expression of subunits of adenosine triphosphate
CC synthase in thermophilic bacterium PS3."
RL Biochim. Biophys. Acta 933:141-155(1988).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
CC THROUGH THE CF(0) COMPLEX.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
CC -----
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CC -----
CC EMBL: X07804; CAA30653.1; -.
CC PIR: S01402; S01402.
CC HSSP: P05631; 1BMF.
CC InterPro: IPR000131; ATPase_gamma.
CC Pfam: PF00231; ATP-synt. 1.
CC PRINTS: PR00126; ATPASEGAMMA.
CC PROSITE: PS00153; ATPASE_GAMMA: 1.
CC KMW Hydrolyase; ATP synthetase; CF(1); Hydrogen ion transport.
CC FT PROPEP 1 286
CC CHAIN 5 286 ATP SYNTHASE GAMMA CHAIN
CC SEQUENCE 286 AA; 32248 MW; ABB96F687C999252 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
DB 212 EILDV 216

RESULT 14
ATPG_BACCA STANDARD: PRT; 287 AA.
AC P41010;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ATP synthase gamma chain (EC 3.6.3.14).
GN ATPG.
OS Bacillus caldotenax.
CC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
CC NCBI_TaxID=1395;
OK NCBI_TaxID=1395;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishizuka M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
CC THROUGH THE CF(0) COMPLEX.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
CC -----
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CC -----
CC EMBL: D38058; BAA07247.1; -.
CC HSSP: P05631; 1BMF.
CC InterPro: IPR000131; ATPase_gamma.
CC Pfam: PF00231; ATP-synt. 1.
CC PRINTS: PR00126; ATPASEGAMMA.
CC PROSITE: PS00153; ATPASE_GAMMA.
CC KMW ATP synthetase; CF(1); Hydrogen ion transport; Hydrolyase.
CC SEQUENCE 287 AA; 32343 MW; BA039503BD1BF1E5A CRC64;

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CC -----
CC EMBL: D38058; BAA07247.1; -.
CC HSSP: P05631; 1BMF.
CC InterPro: IPR000131; ATPase_gamma.
CC Pfam: PF00231; ATP-synt. 1.
CC PRINTS: PR00126; ATPASEGAMMA.
CC PROSITE: PS00153; ATPASE_GAMMA.
CC KMW ATP synthetase; CF(1); Hydrogen ion transport; Hydrolyase.
CC SEQUENCE 287 AA; 32343 MW; BA039503BD1BF1E5A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
DB 213 EILDV 217

RESULT 15
ATPG_BACST STANDARD: PRT; 287 AA.
AC P42007;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ATP synthase gamma chain (EC 3.6.3.14).
GN ATPG.
OS Bacillus stearothermophilus.
CC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Geobacillus.
CC NCBI_TaxID=1422;
OK NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishizuka M., Imai H.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
CC THROUGH THE CF(0) COMPLEX.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
CC -----
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CC -----
CC EMBL: D38060; BAA07254.1; -.
CC HSSP: P05631; 1BMF.
CC InterPro: IPR000131; ATPase_gamma.
CC Pfam: PF00231; ATP-synt. 1.
CC PRINTS: PR00126; ATPASEGAMMA.
CC PROSITE: PS00153; ATPASE_GAMMA.
CC KMW ATP synthetase; CF(1); Hydrogen ion transport; Hydrolyase.
CC SEQUENCE 287 AA; 32391 MW; 78A9FB92ED01BAE6E CRC64;

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OY 1 e1dv 5
|||||
Db 213 E1DV 217

Search completed: June 10, 2002, 06:24:23
Job time: 228 sec

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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:23:50 : Search time 25.42 Seconds
(without alignments)
34.027 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	14	10	P82341
2	23	100.0	50	16	Q927L9
3	23	100.0	70	3	Q9C2D4
4	23	100.0	100	11	Q9DAR8
5	23	100.0	116	11	Q9JXS1
6	23	100.0	117	11	Q9JXS2
7	23	100.0	117	11	Q9JXS0
8	23	100.0	117	11	Q9JXS8
9	23	100.0	119	17	Q28742
10	23	100.0	119	17	Q9HCG9
11	23	100.0	147	16	Q53866
12	23	100.0	171	3	Q9US90
13	23	100.0	172	5	Q9NIV2
14	23	100.0	174	16	Q97IB1
15	23	100.0	176	2	Q9F2I3
16	23	100.0	180	2	Q923N7

17	23	100.0	180	16	Q97OD9	Q97d9 streptococ
18	23	100.0	186	6	Q9M231	Q9m231 bos taurus
19	23	100.0	200	10	Q9STJ1	Q9stj1 arabidopsis
20	23	100.0	208	3	Q13501	Q13501 phanerocha
21	23	100.0	212	4	Q95609	Q95609 homo sapien
22	23	100.0	219	2	Q53253	Q53253 rhizobium t
23	23	100.0	222	16	Q9WY98	Q9wy98 thermotoga
24	23	100.0	226	2	Q9L6U6	Q9l6u6 pseudomonas
25	23	100.0	242	17	Q27260	Q27260 methanococ
26	23	100.0	246	2	Q9FDJ6	Q9fdj6 lactobacill
27	23	100.0	253	16	Q51655	Q51655 borrelia bu
28	23	100.0	256	5	Q44520	Q44520 caenorhabdi
29	23	100.0	266	16	Q92223	Q92223 rhizobium m
30	23	100.0	267	17	Q97WL9	Q97wl9 sulfolobus
31	23	100.0	268	10	Q94BW7	Q94bw7 cicier ariet
32	23	100.0	270	2	Q24845	Q24845 acinetobact
33	23	100.0	271	4	Q9H027	Q9h027 homo sapien
34	23	100.0	271	16	Q53065	Q53065 lactococcus
35	23	100.0	274	11	Q9EQ23	Q9eq23 ratius norv
36	23	100.0	277	11	Q921S2	Q921s2 mus musculu
37	23	100.0	282	2	Q52412	Q52412 thermophil
38	23	100.0	287	16	Q9CN70	Q9cn70 pasteurella
39	23	100.0	289	16	Q92H07	Q92h07 rickettsia
40	23	100.0	290	5	Q17829	Q17829 caenorhabdi
41	23	100.0	307	16	Q9JUD6	Q9jud6 neisseria m
42	23	100.0	307	16	Q9J534	Q9js34 neisseria m
43	23	100.0	308	2	Q9X9K3	Q9x9k3 vibrio para
44	23	100.0	312	3	Q74864	Q74864 schizosacch
45	23	100.0	317	6	Q9GMV1	Q9gmv1 macaca fasc

ALIGNMENTS

RESULT 1

82341 PRELIMINARY: PRT: 14 AA.

AC P82341; 01-JUN-2000 (TREMBLrel. 14, Created)

DR 01-JUN-2000 (TREMBLrel. 14, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE UNKNOWN PROTEIN FROM 2D-PAGE OF THYLAKOID (SPOT251) (FRAGMENT).

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

OX NCBI_TaxID=3888;

RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

RC STRAIN=CV, DE GRACE; TISSUE=LEAF;

RX MEDLINE=20181728; PubMed=10715320;

RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,

RA Adamska I., Van Wijk K.J.;

RT "Proteomics of the chloroplast: systematic identification and

targeting analysis of luminal and peripheral thylakoid proteins.";

RL Plant Cell 12:319-341(2000).

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR

PERIPHERY.

CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.

CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN

PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.

KW Chloroplast; Thylakoid membrane.

FT NON_TER 14

FT SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;

Query Match 100.0%; Score 23; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 eildv 5

Db 7 eildv 11

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RESULT 2
0927L9 PRELIMINARY; PRT; 50 AA.
AC 0927L9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHEICAL 6.0 KDA PROTEIN.
GN CPN0685 OR CPJ0685
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shira M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AF001651; AAD18824.1;
DR EMBL; AP002547; BAA98892.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 50 AA; 5959 MW; 4A8961A037A16495 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elidv 5
Db 7 EILDV 11

RESULT 3
09C2D4 PRELIMINARY; PRT; 70 AA.
AC 09C2D4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHEICAL 7.8 KDA PROTEIN.
GN 966.310.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL513463; CAC28779.2;
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7809 MW; EDAEC64FE6B2E9BC CRC64;

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Query Match 100.0%; Score 23; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elidv 5
Db 7 EILDV 11

RESULT 4
09D4R8 PRELIMINARY; PRT; 100 AA.
AC 09D4R8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 4930568L2IRIK PROTEIN.
GN 4930568L2IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guslinich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016255; BAB30165.1;
DR MGI; MGI:1923108; 4930568L2IRIK.
SQ SEQUENCE 100 AA; 11528 MW; 59CFB27CD19C1112 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elidv 5
Db 93 EILDV 97

RESULT 5
09UKS1 PRELIMINARY; PRT; 116 AA.
AC 09UKS1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE MUTANT C-KIP RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-BROWN NORWAY, TISSUE-TESTIS;
RA Gangadharan S., All S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
male rat testis";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF228308; AAF69131.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA: 12583 MW: 8BD45FB24E2471EC CRC64:

Query Match 100.0%; Score 23; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
DB 75 EILDV 79

RESULT 6
O9JKS2 PRELIMINARY; PRT: 117 AA.

ID O9JKS2
AC 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE C-RT RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BROWN NORWAY, TISSUE-TESTIS, AND BRAIN;
RA Gangadharan S., All S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
male rat testis";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF228307; AAF69130.1; -
DR InterPro: IPR003600; IG_1like.
DR SMART: SM00410; IG_1like; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12635 MW: E2141AF47115EE78 CRC64:

Query Match 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
DB 76 EILDV 80

RESULT 7
O9JKS0 PRELIMINARY; PRT: 117 AA.

ID O9JKS0
AC 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE C-RT RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BROWN NORWAY, TISSUE-TESTIS;
RA Gangadharan S., All S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
male rat testis";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF228308; AAF69132.1; -
DR InterPro: IPR003600; IG_1like.
DR SMART: SM00410; IG_1like; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12611 MW: E7BEC87E579CB678 CRC64:

Query Match 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
DB 76 EILDV 80

RESULT 8
O9JKR8 PRELIMINARY; PRT: 117 AA.

ID O9JKR8
AC 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE C-RT RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BROWN NORWAY, TISSUE-TESTIS;
RA Gangadharan S., All S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
male rat testis";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF228311; AAF69134.1; -
DR InterPro: IPR003600; IG_1like.
DR SMART: SM00410; IG_1like; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12641 MW: F3FBDC2F1288F378 CRC64:

Query Match 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
DB 76 EILDV 80

RESULT 9
O28742 PRELIMINARY; PRT: 119 AA.

ID O28742
AC 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-JUN-1998 (TREMBlrel. 07, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AF1530.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus
OX NCBI_TaxID=2234;

RESULT 10
O9HOG9 PRELIMINARY: PRT: 119 AA.
AC O9HOG9: 100.0%; Score 23; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
DB 109 EILDV 113

SEQUENCE FROM N.A.
RP STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klank H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kierlavague A.R., Graham D.E., Kyrtides N.C.,
RA Faltischnann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon *Archaeoglobus fulgidus*.";
RL Nature 390:364-370(1997).
DR EMBL: AE000997; AAB89718.1; -
DR TIGR: AF1530; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 119 AA; 14025 MW; 7F75DA93E80C15C CRC64;

Query Match 100.0%; Score 23; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
DB 109 EILDV 113

SEQUENCE FROM N.A.
RP MEDLINE=20504483; PubMed=11016950;
RX Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sirogna J.,
RA Lettewell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
RA Lettewell S., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jahnson P.E., Krebs M.P., Angewine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of *Halobacterium* species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AE005045; AAG19546.1; -
KW Complete proteome.
SQ SEQUENCE 119 AA; 13648 MW; 585905ABA983B981 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
DB 110 EILDV 114

RESULT 11
O53866 PRELIMINARY: PRT: 147 AA.
AC O53866: 100.0%; Score 23; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
DB 17 EILDV 21

SEQUENCE FROM N.A.
RP STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL: AL022004; CAA17660.1; -
DR Tuberculist; RV0854; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 147 AA; 16345 MW; DB855F6B86293E07 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 eildv 5
DB 17 EILDV 21

SEQUENCE FROM N.A.
RP STRAIN-968 H90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Harauchi T.,
RA Hiraoaka Y.;
RT "Large-scale screening of intracellular protein localization in living
fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
DR EMBL: AB027955; BAA87259.1; -
KW Nuclear protein.
FT NON_TER 1 1
FT 171 171
SQ SEQUENCE 171 AA; 21395 MW; 30012B18345508BE CRC64;

Query Match 100.0%; Score 23; DB 3; Length 171;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
 |||||
 DB 151 EILDV 155

RESULT 13

09NIV2 PRELIMINARY; PRT: 172 AA.
 AC 09NIV2: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE STELLATE PROTEIN.
 GN STE.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shevel'ov Y.I., Kalmykova A.I.;
 RT "Stellate orpion provides a poly(A) signal for bendless mRNA.";
 RL Submitted (OCF-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF192309; AAF35172.1; -;
 DR FLYBASE: FBgn003523; Ste.
 DR InterPro: IPR00704; CAS_Kinase_II.
 DR Pfam: PF01214; CK_II_beta; 1.
 DR PRINTS: PR00472; CASNMASEII.
 DR PROSITE: PS01101; CK2_BETA; 1.
 SQ SEQUENCE 172 AA; 19525 MW; A2C8752F3A976F8B CRC64;

Query Match 100.0%; Score 23; DB 5; Length 172;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
 |||||
 DB 46 EILDV 50

RESULT 14

097IB1 PRELIMINARY; PRT: 174 AA.
 AC 097IB1: 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE UNCHARACTERIZED CONSERVED PROTEIN (COILED-COIL).
 GN CAC1739.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng O.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitt J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007683; AAK79705.1; -;
 KW Complete proteome.
 SQ SEQUENCE 174 AA; 20244 MW; 80EA9CA386E436BF CRC64;

Query Match 100.0%; Score 23; DB 16; Length 174;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
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 DB 32 EILDV 36

RESULT 15

09F2I3 PRELIMINARY; PRT: 176 AA.
 AC 09F2I3: 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE YLBN-LIKE HYPOTHETICAL PROTEIN.
 GN YLBN-LIKE.
 OS Streptococcus gordonii challis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=29390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHALLIS;
 RA Minick P., Vickerman M.;
 RL Submitted (OCF-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U12643; AAC32547.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 176 AA; 19929 MW; B7E430114725CFF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 32 EILDV 36

Search completed: June 10, 2002, 06:28:04
 Job time: 254 sec

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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:21:15 ; Search time 25.45 Seconds
(without alignments)
21.822 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 e1ldv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1	/SIDS1/gcgdata/genseq/genseqp-emb1/AA1980.DAT *
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22	/SIDS1/gcgdata/genseq/genseqp-emb1/AA2001.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

ET

Result No.	Score	Query Match	Length	DB	ID	Description
1	23	100.0	5	17	AAR95719	Alpha-Beta-1 inter
2	23	100.0	5	18	AAW25192	LDV-peptide capab
3	23	100.0	5	19	AAW45318	Peptide recognisec
4	23	100.0	5	20	AAV03855	Integrin ligand d
5	23	100.0	5	21	AAV80488	Cell adhesion pep
6	23	100.0	5	21	AAV77442	Fibronectin CSI-d
7	23	100.0	5	21	AAV69619	VLA-4 inhibitor pe
8	23	100.0	5	22	AAW73465	Fibronectin VLA-4
9	23	100.0	5	22	AAW91966	Fibronectin fragme
10	23	100.0	5	22	AAW50876	Integrin recogniti
11	23	100.0	5	22	AAW59135	Peptide #3 recogni

12	23	100.0	6	21	AAV7744.3	Fibronectin CSI-de
13	23	100.0	7	19	AAV7744.4	Fibronectin CSI-de
14	23	100.0	7	19	AAV5605	Alpha4 integrins t
15	23	100.0	8	12	AAAR1361	Peptide #352 deriv
16	23	100.0	8	13	AAAR2885	Cell adhesion inh
17	23	100.0	8	15	AAAR4360	Polymer-bound cell
18	23	100.0	8	17	AAAR92536	VLA-4 binding pep
19	23	100.0	8	18	AAW25190	LDV-peptide capab
20	23	100.0	8	19	AAW53133	Peptide sequence o
21	23	100.0	8	19	AAW56046	Chemeric adenoviru
22	23	100.0	8	20	AAV32862	Fibronectin protei
23	23	100.0	8	20	AAV32874	Fibronectin protei
24	23	100.0	8	21	AAAB35774	Vitronectin peptid
25	23	100.0	8	21	AAAB80489	Cell adhesion pep
26	23	100.0	8	21	AAI69618	VLA-4 inhibitor pe
27	23	100.0	8	22	AAAB73464	Fibronectin VLA-4
28	23	100.0	8	22	AAAB91967	Fibronectin fragme
29	23	100.0	9	13	AAAR29631	Adhesion inhibitor
30	23	100.0	9	13	AAAR30433	Cell adhesion inh
31	23	100.0	9	13	AAAR28886	Cell adhesion inh
32	23	100.0	9	21	AAV77436	Fibronectin CSI-de
33	23	100.0	9	21	AAV77437	Fibronectin CSI-de
34	23	100.0	9	21	AAV77438	Fibronectin CSI-de
35	23	100.0	9	21	AAV77439	Fibronectin CSI-de
36	23	100.0	10	13	AAAR25998	Adhesion inhibitor
37	23	100.0	10	13	AAAR30432	Cell adhesion inh
38	23	100.0	10	13	AAAR29103	Platelet aggregati
39	23	100.0	10	13	AAAR29105	Platelet aggregati
40	23	100.0	10	13	AAAR29106	Platelet aggregati
41	23	100.0	10	13	AAAR29107	Platelet aggregati
42	23	100.0	10	13	AAAR29108	Platelet aggregati
43	23	100.0	10	13	AAAR29109	Platelet aggregati
44	23	100.0	10	16	AAW01705	Standard peptide f
45	23	100.0	10	16	AAW01725	Inhibitor of fibro

ALIGNMENTS

RESULT 1

ID AAR95719 standard; peptide; 5 AA.

AC AAR95719;

DT 04-DEC-1996 (first entry)

Alpha-4Beta-1 integrin binding inhibitory peptide 16

VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;

KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;

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FT	Modified-site	5	1
FT	Modified-site	5	1

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DN 1165510333-2XX
XX
33-APP-1006

XX 07-THU-1004. 0411C-0271830
DE

XX 07-TRT-1004. 94116-0371030
BP

XX
XX
(TEVA-) TEVAC BIOLOGY CORP

XX	Koran	ED	Bog	Vanderl
DT				

XX
DB
FBI: 1006-321374/33

XX New peptide(s) based on the LDV domain of fibronectin - used for
 PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
 PT fibronectin or invasion
 XX
 PS Disclosure; Column 21-22; 35pp; English.
 XX
 CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
 CC surface of endothelial cells that line the interior wall of capillaries.
 CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
 CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
 CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
 CC white blood cells to adhere to the capillary wall in areas where the
 CC tissue surrounding the capillary has been infected or damaged. Sometimes
 CC this white blood cell migration can become uncontrolled, with white
 CC blood cells flooding to the scene, causing widespread tissue damage.
 CC Ccgs. capable of blocking this process may be beneficial as therapeutic
 CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
 CC fibronectin. Three distinct IA4B1-binding sites have been identified
 CC within fibronectin. One site is found in the HepII region and is
 CC expressed in all isoforms; two others (CS1 and CS5) are present in the
 CC alternatively spliced type III connecting segments. CS1 has the higher
 CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
 CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
 CC peptide that include the LDV domain presented in such a way by its novel
 CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
 CC
 SQ Sequence 5 AA:

Query Match 100.0%; Score 23; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 eildv 5
 |||||
 Db 1 eildv 5

RESULT 2

AAW25192
 ID AAW25192 standard; peptide; 5 AA.
 XX

AC AAW25192;

DT 05-JAN-1998 (first entry)

DE LDV-peptide capable of binding cell adhesion molecules.

XX LDV; leucine; aspartic acid; valine; cell adhesion molecule;

KW binding; bladder irrigation; tumour removal; endoscopic operation;
 KW transurethral resection; cancer; neoplasia.

XX Synthetic.

OS
 XX
 PN DE19529909-A1.

PD 20-FEB-1997.

PF 15-AUG-1995; 95DE-1029909.

PR 15-AUG-1995; 95DE-1029909.

PA (FREP) FRESENIUS AG.

XX Boehle A;

DR WPI; 1997-133793/13.

XX Endoscopic irrigation soins. - contg. peptide(s) that bind to cell
 PT adhesion molecules
 XX

PS Claim 6; Page 8; 8pp; German.

XX AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
 CC The peptides are capable of binding to cell adhesion molecules and
 CC are used in aqueous irrigation solutions for use during and after
 CC endoscopic operations. Preferred irrigation solutions are
 CC electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
 CC oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
 CC GPRP, VRL, YIGSR, KOADV and/or REDV (given in one letter amino acid
 CC code). The solutions are especially used for irrigating the bladder
 CC during and after tumour removal by transurethral resection. The
 CC peptides protect against recurrence of tumours.
 CC
 SQ Sequence 5 AA:

Query Match 100.0%; Score 23; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 eildv 5
 |||||
 Db 1 eildv 5

RESULT 3

AAW6318
 ID AAW6318 standard; Protein; 5 AA.
 XX

AC AAW6318;

DT 08-MAY-1998 (first entry)

DE Peptide recognised by integrin alpha4beta1.

XX Fibronogen; integrin; alpha-IIB-beta3; cell surface receptor;

KW penton base protein; coat proteins; adenovirus; binding site;
 KW cellular adhesion; extracellular matrix molecule; binding domain;
 KW cell surface binding site; Dispecific molecule; gene therapy.

XX Unidentified.

OS
 XX
 PN US5712136-A.

PD 27-JAN-1998.

PF 17-APR-1996; 96US-0634060.

PR 08-SEP-1994; 94US-0303162.

XX (GENV-) GENVEC INC.

PA Brough DE, Bruder JT, Kovesdi I, McVey DL, Roelvink PW;
 PI Wickham TJ;

XX WPI; 1998-119984/11.

XX Methods for introducing adenovirus into cells - used for genetic
 PT engineering and gene therapy
 PT
 XX

PS Claim 27; Column 2; 56pp; English.

XX The present sequence is a linear stretch of amino acids (present in
 CC fibronectin) recognised by the integrin alpha4beta1. Integrins are
 CC cell surface receptors. The penton base protein (one of the coat
 CC proteins) of adenoviruses binds to integrins. The integrins not only
 CC provide a binding site for the adenoviral penton base protein, but also
 CC mediate cellular adhesion to the extracellular matrix molecules. The
 CC specification describes a method of introducing an adenovirus into
 CC a cell in vitro having a particular cell surface binding site. The
 CC adenovirus is contacted with a bispecific molecule comprising a component
 CC that selectively binds a binding domain of the penton base protein of the
 CC adenovirus and a second component that selectively binds the cell surface
 CC binding site. A complex of the adenovirus and the bispecific molecule is

CC formed, and the cell is contacted with it to allow entry of the
CC adenovirus into the cell. The methods can be used for research and the
CC vectors can be used for gene therapy.

XX
SQ Sequence 5 AA:

Query Match 100.0%; Score 23; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
Db 1 elldv 5

RESULT 4

AAV03855
ID AAV03855 standard; peptide: 5 AA.

XX
AC AAV03855;

XX
DT 16-JUN-1999 (first entry)

XX
DE Integrin ligand dissociator (ILD) peptide.

XX Integrin-11gand; dissociator; disaggregation; platelet thrombus; stroke;
KW fibrinogen; glycoprotein IIb-IIIa; angina; myocardial infarction; bone;
KW osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
KW periclast; tumor; atherosclerosis; inflammatory bowel disease; asthma;
KW organ transplant rejection; arthritis; ILD.

XX
OS Synthetic.

XX
PN WC9911280-A1.

XX
PD 11-MAR-1999.

XX
PF 03-SEP-1998; 98WO-US18305.

XX
PR 03-SEP-1997; 97US-0057463.

XX
PA (BURN-) BURNHAM INST.

XX
PI Hu DD, Smith JW;

XX
DR WPI: 1999-243586/20.

XX
PT Disaggregating a ligand: integrin receptor complex

XX
PS Disclosure; Page 10; 39pp; English.

XX The invention relates to integrin ligand dissociators. Disaggregation of
CC an existing platelet thrombus in a blood vessel is due to dissociation of
CC fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the
CC binding of an integrin-11gand dissociator at ligand binding site 1 of
CC glycoprotein IIb-IIIa. The invention provides a method of disaggregating
CC an existing platelet thrombus in a blood vessel, where the platelet
CC thrombus may form an occlusion of a blood vessel, in a subject comprises
CC administering a compound which dissociates fibrinogen bound to a first
CC site on platelet glycoprotein IIb-IIIa, by binding to a second
CC interacting site on platelet glycoprotein IIb-IIIa, disaggregating the
CC platelet thrombus. The method is used to treat humans with unstable
CC angina, stroke and/or acute myocardial infarction. The methods can be
CC used to enact de-adhesion of osteoclasts from the bone surface to halt
CC bone loss in a patient with osteoporosis. The methods can also be used
CC for the de-adhesion of angiogenic endothelial cells in a patient with a
CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
CC retinopathy, psoriasis. The methods can also be used to treat tumors,
CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
CC bowel disease, or organ transplant rejection, and asthma. The methods can
CC be used for the dissolution of pre-formed platelet aggregates, which is a
CC departure from the current strategy of treatment prior to formation of

CC vascular occlusions. The present sequence represents an integrin ligand
CC dissociator (ILD) that can be used in the method of the invention.

XX
SQ Sequence 5 AA:

Query Match 100.0%; Score 23; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
|||||
Db 1 elldv 5

RESULT 5

AAV80488
ID AAV80488 standard; peptide: 5 AA.

XX
AC AAV80488;

XX
DT 06-JUN-2000 (first entry)

XX
DE Cell adhesion peptide #23.

XX Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.

XX
OS Synthetic.

XX
PN WO200004941-A1.

XX
PD 03-FEB-2000.

XX
PF 22-JUL-1999; 99WO-US16800.

XX
PR 24-JUL-1998; 98US-0122348.

XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.

XX
PI Budny JA;

XX
DR WPI: 2000-195084/17.

XX
PT System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption

XX
PS Claim 14; Page 32; 44pp; English.

XX The invention relates to a novel system for reconstruction of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes
CC bone formation and a component that decreases bone resorption (II).
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (I) is preferably selected from: selectin or selectin binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC plasminogen activator inhibitors, protease inhibitors and
CC metalloprotease inhibitors. The peptides AAV80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (I) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.

XX
SQ Sequence 5 AA:

Query Match 100.0%; Score 23; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 eildv 5
Db 1 eildv 5

RESULT 6
AAV77442

ID AAV77442 standard; peptide: 5 AA.

AC AAV77442;

DT 22-MAY-2000 (first entry)

DE Fibronectin CS1-derived peptide #33.

KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
CD9d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.

OS Mammalia.

PN WO200002903-A1.

PD 20-JAN-2000.

PF 15-DEC-1998; 98WO-US26605.

PR 10-JUL-1998; 98US-0113689.

PA (CYTE-) CYTEL CORP.

PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;

DR WPI: 2000-182213/16.

PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders -
XX
XX
PS Disclosure: Fig 2; 243pp; English.

XX The invention relates to peptidomimetic compounds (AAV77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD9d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4 mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAV77411-Y77414
CC and AAV77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAV77410).

SQ Sequence 5 AA;

Query Match, 100.0%; Score 23; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 eildv 5
Db 1 eildv 5

RESULT 7
AAV69619

ID AAV69619 standard; peptide: 5 AA.

AC AAV69619;

DT 19-APR-2000 (first entry)

DE VLA-4 inhibitor peptide #2.

KW LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
CD9d/CD29; cell adhesion; arylalkyl azolyalkanoic acid derivative;
arylureidoalkyl azolyalkanoic acid derivative; inflammatory disorder;
autoimmune disorder; respiratory disorder; LDV motif.

OS Synthetic.

PN WO200000477-A1.

PD 06-JAN-2000.

PF 31-MAY-1999; 99WO-IB00973.

PR 30-JUN-1998; 98US-0091180.

PA (PFIZ) PFIZER PROD INC.

PI Duplantier AJ, Milici AJ, Chupak LS;

DR WPI: 2000-126762/11.

PT Arylalkyl and arylureidoalkyl azolyalkanoic acid derivatives -
PT
XX
XX
PS Disclosure: Page 2; 120pp; English.

XX The invention relates to novel arylalkyl and arylureidoalkyl
CC azolyalkanoic acid derivatives and related compounds (1), and their
CC salts and prodrugs. These are are integrin inhibitors, specifically of
CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
CC inducible cell surface protein VCAM-1 (vascular cell adhesion
CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
CC and consequent or associated pathogenic processes mediated by VLA-4, and
CC may therefore be useful in the treatment and prevention of inflammatory,
CC autoimmune, or respiratory disorders. These include asthma, arthritis,
CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
CC inflammatory bowel disease. Sequences AAV69618-Y69620 represent peptides
CC derived from the VLA-4-binding domain of the FN CS-1 region which
CC contain the LDV motif and are known to inhibit fibronectin-dependent
CC cell adhesion.

SQ Sequence 5 AA;

Query Match
Best Local Similarity 100.0%; Score 23; DB 21; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
Db 1 eildv 5

RESULT 8

AAB73465
ID AAB73465 standard; peptide: 5 AA.
XX
AC AAB73465:
XX
DT 02-JUN-2001 (first entry)
XX
DE Fibrinectin VLA-4 binding domain-derived pentapeptide #1.
XX
KW Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
KW very late antigen; antibody; kidney disease; chronic renal failure;
KW end-stage renal disease; chronic diabetic nephropathy;
KW diabetic glomerulopathy; diabetic renal hypertrophy;
KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
KW nephrotropic; cell adhesion inhibition; fibrinectin CS-1 region.
XX
OS Unidentified.
XX
PN WO200119396-A1.
XX
PD 22-MAR-2001.
XX
PE 14-SEP-2000: 2000WO-US25140.
XX
PR 14-SEP-1999: 99US-0153826.
XX
PA (BIOJ) BIOGEN INC.
PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX
PI Allen A, Pusey C, Lobb R;
XX
DR WPI: 2001-273408/28.
XX
PT Treating a mammal in, or at a risk of developing, chronic renal
PT failure, involves administering at least one integrin antagonist to the
PT mammal -
XX
PS Disclosure: Page 24; 62pp; English.
XX
CC The invention relates to a method for treating a mammal with,
CC or at risk of developing, chronic renal failure, involving the
CC administration of at least one integrin antagonist. The integrin
CC antagonists that may be used in the method include antagonists of
CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
CC containing integrins. In particular, the antagonists are antibodies
CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
CC the case of VLA-1, and fibrinectin and VCAM-1 in the case of VLA-4).
CC The method of the invention may be used to treat chronic renal failure,
CC end-stage renal disease, chronic diabetic nephropathy, diabetic
CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
CC peptides derived from the VLA-4 binding domain (CS-1 region) of
CC fibrinectin, which inhibit fibrinectin-dependent cell adhesion, and may
CC therefore be used in the method of the invention.
XX
SO Sequence 5 AA:
XX
Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 elldv 5
DB 1 elldv 5
RESULT 9
AAB91966

ID AAB91966 standard; Peptide: 5 AA.
XX
AC AAB91966:
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1142.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PE 17-MAY-2000: 2000WO-US13576.
XX
PR 17-MAY-1999: 99US-0134406.
PR 10-SEP-1999: 99US-0153406.
PR 15-OCT-1999: 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure: Page 569; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (II) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SO Sequence 5 AA:
XX
Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 elldv 5
DB 1 elldv 5
RESULT 10
AAB50876
ID AAB50876 standard; peptide: 5 AA.
XX
AC AAB50876:
XX

DT 19-MAR-2001 (first entry)
XX Integrin recognition peptide sequence #3.
DE XX
XX Integrin; transmembrane protein; alpha4 integrin inhibitor;
KW Paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
XX Multiple sclerosis; asthma; atherosclerosis; wound healing.
OS Unidentified.
XX
XX WO200073342-A1.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 01-JUN-2000; 2000WO-US15153.
PF
XX
XX 01-JUN-1999; 99US-0323447.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Ginsberg MH, Pfaff M, Liu S;
PI
XX
XX WPI; 2001-070959/08.
DR
XX
XX Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT heptad repeats -
XX
XX
XX Disclosure; Page 2; 37pp; English.
PS
XX
XX The present sequence is given in a specification relating to a
CC polypeptide comprising a series of heptad-repeats that mimic a
CC transmembrane domain, and a selected cytoplasmic domain attached to the
CC heptad repeats. At least a portion of the polypeptide is prepared
CC recombinantly or at least 1 heptad repeat in the series has a different
CC amino acid sequence to other heptad repeats in the series. The
CC polypeptide is useful in the construction of structural models which are
CC useful for evaluating structure and activity of a selected occupied and
CC clustered transmembrane protein having the selected cytoplasmic domain
CC and for identifying therapeutic compounds. It is also useful for
CC identifying agents as inhibitors of alpha4 integrin biological
CC responses by contacting the structural model with paxillin or a
CC paxillin related molecule in the presence and absence of a test agent
CC and determining binding of paxillin or paxillin related molecule to the
CC structural model. A decrease in binding in the presence of the test
CC agent indicates that the test agent is an inhibitor of alpha4 integrin
CC biological response. Inhibitors of the binding of paxillin to alpha4 are
CC useful in blocking immune responses in conditions such as inflammatory
CC bowel disease, arthritis, multiple sclerosis and asthma and in
CC inhibiting atherosclerosis and scarring during wound healing.
CC
XX
XX Sequence 5 AA:
SQ

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|
|
|
|
|
Db 1 eildv 5

RESULT 11
AAB59135
ID AAB59135 standard; peptide: 5 AA.
XX
XX AAB59135;
AC
XX
XX 21-MAR-2001 (first entry)
DT
XX
XX Peptide #3 recognised by integrin.
DE

XX
XX Heptad repeat; transmembrane domain; cytoplasmic; integrin;
KW inflammation; thrombosis; malignancy.
DE XX
XX Synthetic.
OS
XX WO200073341-A1.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 26-MAY-2000; 2000WO-US14656.
PF
XX
XX 27-MAY-1999; 99US-0320907.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Ginsberg MH, Pfaff M;
PI
XX
XX WPI; 2001-041143/05.
DR
XX
XX Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT the repeats -
XX
XX
XX Disclosure; Page 2; 36pp; English.
PS
XX
XX The present invention relates to a peptide with a series of
CC heptad-repeats that mimic a transmembrane domain and a selected
CC cytoplasmic domain attached to the heptad repeats. The invention
CC is useful for evaluating structure and activity of a selected
CC occupied and clustered transmembrane protein with the selected
CC cytoplasmic domain and for identifying therapeutic compounds. It
CC is also useful for identifying a cytoplasmic domain binding partner.
CC It is may be used to study protein interactions with transmembrane
CC proteins such as integrin, which can be used to treat conditions in
CC which over activity of integrins is involved, such as inflammation,
CC thrombosis and malignancy.
CC
XX
XX Sequence 5 AA:
SQ

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|
|
|
|
|
Db 1 eildv 5

RESULT 12
AAV77443
ID AAV77443 standard; peptide: 6 AA.
XX
XX AAV77443;
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Fibronection CS1-derived peptide #34.
DE
XX
XX Fibronection; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
XX Mammalia.
OS
XX
XX WO200002903-A1.
PN
XX
XX 20-JAN-2000.
PD
XX
XX 15-DEC-1998; 98WO-US26605.
PF
XX

PR 10-JUL-1998; 98US-0113689.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Arrhenius TS, Ellices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX WPI: 2000-182213/16.
DR
XX
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders
XX
XX
PS Disclosure: Fig 2; 243pp; English.
XX
XX The invention relates to peptidomimetic compounds (AAV77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD9d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAV77411-Y77414
CC and AAV77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAV77410).
XX
XX
SQ Sequence 6 AA:

Query Match 100.0%; Score 23; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 elldv 5
 |||||
DB 2 elldv 6

RESULT 13
AAV77444
ID AAV77444 standard; peptide: 6 AA.
XX
XX AAV77444:
AC
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CS1-derived peptide #35.
XX
XX Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD9d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
XX Mammalia.
OS
XX
PN WO200002903-A1.
XX
PD 20-JAN-2000.
XX
PF 15-DEC-1998; 98WO-US26605.
XX

PR 10-JUL-1998; 98US-0113689.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Arrhenius TS, Ellices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX WPI: 2000-182213/16.
DR
XX
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders
XX
XX
PS Disclosure: Fig 2; 243pp; English.
XX
XX The invention relates to peptidomimetic compounds (AAV77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD9d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAV77411-Y77414
CC and AAV77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAV77410).
XX
XX
SQ Sequence 6 AA:

Query Match 100.0%; Score 23; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 elldv 5
 |||||
DB 1 elldv 5

RESULT 14
AAW56065
ID AAW56065 standard; peptide: 7 AA.
XX
XX AAW56065:
AC
XX
DT 29-JUL-1998 (first entry)
XX
DE Alpha4 Integrin targeting sequence SEQ ID NO:80.
XX
XX Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW constrained peptide motif; gene therapy; cancer; heart disease;
KW autoimmune disorder.
XX
XX Synthetic.
OS
XX Mastadenovirus.
XX
PN WO9807865-A1.
XX
PD 26-FEB-1998.
XX
PF 21-AUG-1997; 97WO-US14719.
XX

XX 21-AUG-1996; 96US-0701124.
 PR (GENV-) GENVEC INC.
 PA Kovesdi I, Roelivink PW, Wickham TJ;
 XX WPI; 1998-169169/15.
 DR
 PT Chimeric adenovirus fibre proteins - containing non-native amino
 PT acid sequence to provide for binding and entry into cells,
 PT especially for gene therapy
 XX
 PS Example 8; Page 57; 124pp; English.
 XX
 CC The present sequence represents an alpha4 integrins targeting sequence,
 CC which is used in an example from the present invention. The present
 CC invention describes a chimeric adenovirus fibre protein (AFP) containing
 CC a constrained non-native amino acid sequence. The non-native amino acid
 CC sequence allows the chimeric fibre (or a vector comprising the chimeric
 CC fibre) to more efficiently bind to and enter cells. The products can be
 CC used for gene therapy, for treating cancer, e.g. melanoma, glioma and
 CC lung cancers as well as genetic disorders, e.g. cystic fibrosis,
 CC hemophilia and muscular dystrophy as well as pathogenic infections,
 CC e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g.
 CC prevent restenosis following angioplasty or to promote angiogenesis to
 CC reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's
 CC disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
 CC
 SO Sequence 7 AA;

Query Match 100.0%; Score 23; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
 |||||
 Db 1 elldv 5

RESULT 15

AA011361
 ID AA011361 standard; peptide: 8 AA.

AC AA011361;

DT 04-JUN-1991 (first entry)

DE Peptide #352 derived from Cs-1 peptide of IIICS region.

XX Fibronectin; extracellular matrix receptor; ECMR: type III;
 KW connecting segment; IIICS; adhesion; alpha4beta1; lymphocyte;
 KW autoimmune disease; allergy; asthma; ligand.
 XX

OS Synthetic.

XX WO9103252-A.

PD 21-MAR-1991.

PF 31-AUG-1990; 90WO-US04978.

PR 01-SEP-1989; 89US-0402389.

PA (WAYN/) WAYNER E.

PI Wayner E;

DR WPI; 1991-101865/14.

PT Inhibition of lymphocyte adherence to vascular endothelium -
 PT using a novel antibody or peptide for treatment of auto-immune

PT disease, asthma, allergy etc.
 XX
 PS Claim 10; Page 74; 92pp; English.

XX The peptide is derived the Cs-1 peptide (Humphries et al., 1987,
 CC J. Biol. Chem. 262:6886-6892), from the IIICS variable region of
 CC fibronectin. The peptide inhibits binding of lymphocytes to
 CC endothelial cells preventing migration through the vascular
 CC endothelium and into tissues. It acts by blocking the alpha4-
 CC beta1 extracellular matrix receptor. Admin. of the peptide can
 CC suppress the immune response and treat diseases associated with
 CC chronic or relapsing activation of the immune system, including
 CC collagen vascular diseases and other autoimmune diseases,
 CC multiple sclerosis, asthma, allergy and chronic inflammatory skin
 CC conditions.
 CC
 SO Sequence 8 AA;

Query Match 100.0%; Score 23; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 elldv 5
 |||||
 Db 1 elldv 5

Search completed: June 10, 2002, 06:25:07
 Job time: 232 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:36:37 : Search time 14.32 Seconds
(without alignments)
33.551 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 e11dv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	43.5	4	2 A61300	22K superhelical D
2	10	43.5	4	2 PT0624	T-cell receptor be
3	10	43.5	4	2 PT0624	metallothionein-A
4	8	34.8	4	2 E51049	synaptosomal-assoc
5	8	34.8	4	2 E44823	cholecystokinin-5
6	8	34.8	5	2 A32516	20K protein - Rick
7	7	30.4	4	2 B31836	protein-glutamine
8	7	30.4	4	2 A26209	zinc-binding prote
9	7	30.4	5	2 S55237	ig heavy chain CRD
10	7	30.4	5	2 PT0278	biotin A - Citroba
11	6	26.1	4	2 I40697	protein D - Escher
12	6	26.1	4	2 A41890	hypothetical prote
13	6	26.1	4	2 D41654	achatin-I - giant
14	6	26.1	4	2 A32480	ig heavy chain CRD
15	6	26.1	4	2 B53284	T-cell receptor be
16	6	26.1	4	2 I54357	schwannomn - mous
17	6	26.1	4	2 PT0686	T-cell receptor be
18	6	26.1	4	2 PT0711	T-cell receptor be
19	6	26.1	4	2 A60521	glycogen phosphory
20	6	26.1	5	2 C23751	spinal cord peptid
21	6	26.1	5	2 A26830	mitosis inhibiting
22	6	26.1	5	2 B37325	pap fibrillar regul
23	6	26.1	5	2 A32014	tram protein - Esc
24	6	26.1	5	2 B60274	major protein anti
25	6	26.1	5	2 D60274	endo-1,4-beta-xyla
26	6	26.1	5	2 S70615	hypothetical prote
27	6	26.1	5	2 T14908	photosystem I 10.4
28	6	26.1	5	2 P00689	fulicin - giant Af
29	6	26.1	5	2 A44692	

30	6	26.1	5	2 PT0267	ig heavy chain CRD
31	6	26.1	5	2 PT0281	ig heavy chain CRD
32	6	26.1	5	2 PT0308	ig heavy chain CRD
33	6	26.1	5	2 PT0596	T-cell receptor be
34	6	26.1	5	2 PT0513	T-cell receptor be
35	6	26.1	5	2 PT0600	T-cell receptor be
36	6	26.1	5	2 PT0729	T-cell receptor be
37	6	26.1	5	2 PT0601	T-cell receptor be
38	6	26.1	5	2 PT0672	T-cell receptor be
39	6	26.1	5	2 PT0660	T-cell receptor be
40	6	26.1	5	2 PT0651	T-cell receptor be
41	6	26.1	5	2 PT0656	T-cell receptor be
42	6	26.1	5	2 PT0535	T-cell receptor be
43	6	26.1	5	2 PT0639	T-cell receptor be
44	6	26.1	5	2 PT0538	T-cell receptor be
45	6	26.1	5	2 PT0561	T-cell receptor be
46	6	26.1	5	2 PT0540	T-cell receptor be
47	6	26.1	5	2 PT0703	T-cell receptor be
48	6	26.1	5	2 PT0690	T-cell receptor be
49	6	26.1	5	2 PT0573	T-cell receptor be
50	6	26.1	5	2 PT0580	T-cell receptor be
51	6	26.1	5	2 PT0679	T-cell receptor be
52	6	26.1	5	2 S68326	blood cell protein
53	6	26.1	5	2 S69237	surface protein te
54	6	26.1	3	2 A33802	thyrotropin-releas
55	6	21.7	3	2 A37832	phenol 2-monooxyge
56	6	21.7	4	2 I57745	D-mannomate hydrol
57	6	21.7	4	2 B43848	cell surface adhes
58	6	21.7	4	2 I40505	hypothetical prote
59	6	21.7	4	2 I40804	endoglucanase F -
60	6	21.7	4	2 A27887	glucan 1,4-alpha-g
61	6	21.7	4	2 PT0677	T-cell receptor be
62	6	21.7	4	2 S55238	palidipin - assas
63	6	21.7	5	2 JN0862	peptidyl-dipeptida
64	5	21.7	5	2 B41225	copper resistance
65	5	21.7	5	2 B22565	R-phycoerythrin al
66	5	21.7	5	2 T14910	hypothetical prote
67	5	21.7	5	2 A33882	cadmium-binding pe
68	5	21.7	5	2 B37988	acid proteinase II
69	5	21.7	5	2 B45525	actin I - malaria
70	5	21.7	5	2 B61168	cocoonase (EC 3.4.
71	5	21.7	5	2 J70530	ig kappa chain V-I
72	5	21.7	5	2 B44823	synaptosomal-assoc
73	5	21.7	5	2 D44823	synaptosomal-assoc
74	5	21.7	5	2 PT0610	T-cell receptor be
75	5	21.7	5	2 PT0684	T-cell receptor be
76	4	17.4	3	2 P00010	angiotensin-conver
77	4	17.4	3	2 T13892	cytochrome-c oxida
78	4	17.4	4	2 S18401	thyroglobulin - do
79	4	17.4	4	2 A32039	tyrosine-melanocyt
80	4	17.4	4	2 A48360	gamma subunit of P
81	4	17.4	4	2 T46627	hypothetical prote
82	4	17.4	4	2 S09478	globulin IV alpha
83	4	17.4	4	2 S17255	ribosomal protein
84	4	17.4	4	2 T30569	hypothetical prote
85	4	17.4	4	2 I38888	COI Inton 16 prot
86	4	17.4	4	2 A53779	neuropeptide Antho
87	4	17.4	4	2 PT0240	ig heavy chain CRD
88	4	17.4	4	2 A53284	T-cell receptor be
89	4	17.4	4	2 PT0645	T-cell receptor be
90	4	17.4	4	2 PT0633	T-cell receptor be
91	4	17.4	4	2 PT0551	T-cell receptor be
92	4	17.4	4	2 PT0697	T-cell receptor be
93	4	17.4	4	2 PT0721	T-cell receptor be
94	4	17.4	4	2 A40135	branched-chain-emi
95	4	17.4	5	2 S47552	ubiquitin - rat
96	4	17.4	5	1 HOR09A	proctolin - Americ
97	4	17.4	5	2 JN0860	peptidyl-dipeptida
98	4	17.4	5	2 C41225	copper resistance
99	4	17.4	5	2 I40702	primase - Citrobac
100	4	17.4	5	2 E42364	flagellar protein

ALIGNMENTS

RESULT 1

A61300

22K superhelical DNA-binding protein - Escherichia coli (fragment)

C:Species: Escherichia coli

C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C:Accession: A61300

R:Kishl, F.; Edina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.

J. Biochem. 92, 1059-1068, 1982

A:Title: Purification and characterization of a protein from Escherichia coli which form

A:Reference number: A61300; MUID:83082696

A:Accession: A61300

A:Molecule type: protein

A:Residues: 1-4 <KIS>

C:Comment: This protein resembles some of the histone-like protein of bacteria in amino

C:Keywords: DNA binding; monomer

Query Match

Best Local Similarity 43.5%; Score 10; DB 2; Length 4;
Matches 2; Conservative 1; Mismatches 0; Indels 0;

OY 1 eil 3

Db 2 EIV 4

RESULT 2

PT0624

T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0624

R:Reeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601

A:Accession: PT0624

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <PEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 43.5%; Score 10; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 3 ld 4

Db 4 LD 5

RESULT 3

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me

A:Reference number: I51049; MUID:95324545

A:Accession: I51049

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:CrossReferences: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 34.8%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

OY 3 ld 4

Db 1 MD 2

RESULT 4

E44823

synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)

N:Alternate names: superprotein peptide 1

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996

C:Accession: E44823

R:Lowey, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein)

A:Reference number: A44823; MUID:92044785

A:Accession: E44823

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <LOE>

A:Experimental source: visual tissue

A>Note: sequence extracted from NCBI backbone (NCBIP:64247)

C:Keywords: membrane trafficking

Query Match

Best Local Similarity 34.8%; Score 8; DB 2; Length 4;
Matches 1; Conservative 2; Mismatches 0; Indels 0;

OY 2 lld 4

Db 1 IME 3

RESULT 5

A32516

cholecystokinin-5 - dog

N:Alternate names: CCK-5

C:Species: Canis lupus familiaris (dog)

C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000

C:Accession: A32516

R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J

Am. J. Physiol. 252, G272-G275, 1987

A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in

A:Reference number: A32516; MUID:87153871

A:Accession: A32516

A:Molecule type: protein

A:Residues: 1-5 <SHI>

C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy

C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; neuropeptide

F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match

Best Local Similarity 34.8%; Score 8; DB 2; Length 5;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

OY 3 ld 4

Db 3 MD 4

RESULT 6

B31836

20K protein - Rickettsia rickettsii (fragment)

C:Species: Rickettsia rickettsii

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999

C:Accession: B31836

R.Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A:Title: Expression of the gene encoding the 17-kilodalton antigen from *Rickettsia rickettsiae*
A:Reference number: A91885; MUID:89008059
A:Accession: B31836
A:Molecule type: DNA
A:Residues: 15 <AND>
A:Cross-references: GB:J03371; NID:g152455; PIDN:AAD15030.1; PID:g4262874

Query Match 34.8%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 1d 4
DB 1 MD 2

RESULT 7
A26209
Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig (fragment)
C:Species: *Cavia porcellus* (guinea pig)
C>Date: 10-Sep-1987 #sequence-revision 10-Sep-1987 #text-change 03-Mar-1995
C:Accession: A26209
R:Connellan, J.M.; Chung, S.I.; Whetzel, N.K.; Bradley, L.M.; Folk, J.E.
J. Biol. Chem. 246, 1093-1098, 1971
A:Title: Structural properties of guinea pig liver transglutaminase.
A:Reference number: A26209; MUID:71111415
A:Accession: A26209
A:Molecule type: Protein
A:Residues: 1-4 <CON>
A:Experimental source: Liver
C:Keywords: aminocyltransferase

Query Match 30.4%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 dv 5
DB 3 DL 4

RESULT 8
S55237
zinc-binding protein ZBP14 - maize (fragment)
C:Species: *Zea mays* (maize)
C>Date: 27-Oct-1995 #sequence-revision 03-Nov-1995 #text-change 07-May-1999
C:Accession: S55237
R:Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A:Title: Expression and characterization of maize ZBP14, a member of a new family of zinc-binding proteins.
A:Reference number: S55237; MUID:95234046
A:Accession: S55237
A:Molecule type: Protein
A:Residues: 1-5 <ROB>

Query Match 30.4%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 1l 3
DB 4 VL 5

RESULT 9
PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C:Species: *Homo sapiens* (man)

C>Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change 16-Aug-1996
C:Accession: PT0278
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0278
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 30.4%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 1l 3
DB 4 VL 5

RESULT 10
I40697
biotin A - *Citrobacter freundii* (fragment)
C:Species: *Citrobacter freundii*
C>Date: 12-Aug-1996 #sequence-revision 12-Aug-1996 #text-change 12-Aug-1996
C:Accession: I40697
R:Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of *Escherichia coli*, *Citroba*
A:Reference number: I40697; MUID:89006280
A:Accession: I40697
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:M21922; NID:g144434

Query Match 26.1%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
DB 3 D 3

RESULT 11
A41890
Protein D - *Escherichia coli* (fragment)
C:Species: *Escherichia coli*
C>Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change 30-Sep-1993
C:Accession: A41890
R:Sletten, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindqvist, B.H.
J. Bacteriol. 174, 4094-4100, 1992
A:Title: *Escherichia coli* K-12 and B contain functional bacteriophage P2 *ogr* genes.
A:Reference number: A41890; MUID:92283767
A:Accession: A41890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <SLB>
A:Cross-references: GB:M81463

Query Match 26.1%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
DB 2 D 2

RESULT 12

D41654

hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)

C:Species: Haemophilus parainfluenzae

C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995

C:Accession: D41654

R:Kroll, J.S.; Langford, P.R.; Loynds, B.M.

J. Bacteriol. 173, 7449-7457, 1991

A:Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para

A:Reference number: A41654; MUID:92041655

A:Accession: D41654

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 <KRO>

Query Match 26.1%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4

Db 1 D 1

RESULT 13

A32480

achatin-I - giant African snail

C:Species: Achatina fulica (giant African snail)

C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999

C:Accession: A32480

R:Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sur

Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989

A:Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru

A:Reference number: A32480; MUID:89273551

A:Accession: A32480

A:Molecule type: protein

A:Residues: 1-4 <KAM>

A>Note: stereochemistry of the active form confirmed by chemical synthesis

R:Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto

FEBS Lett. 307, 253-256, 1992

A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro

A:Reference number: A44691; MUID:92354723

A:Contents: annotation: X-ray crystallography, 0.85 angstroms

A>Note: achatin-II has L-phenylalanine

C:Keywords: D-amino acid

F;2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 26.1%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4

Db 4 D 4

RESULT 14

PT0271

Ig heavy chain CDR3 region (clone 3-103A) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0271

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0271

A:Molecule type: DNA

A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 26.1%; Score 6; DB 2; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4

Db 1 D 1

RESULT 15

B53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: B53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germ-line diversity an

A:Reference number: A53284; MUID:91342695

A:Accession: B53284

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 <HAR>

A:Cross-references: GB:S60737; NID:9233916; PIDN:AA19518.1; PID:9233918

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60738)

C:Keywords: T-cell receptor

Query Match 26.1%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4

Db 1 D 1

RESULT 16

I54357

schwannomin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I54357

R:Huyhn, D.P.; Nechiporuk, T.; Pulst, S.

Hum. Mol. Genet. 3, 1075-1079, 1994

A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are

A:Reference number: I54357; MUID:95072570

A:Accession: I54357

A>Status: preliminary; translated from GB/EMBL/DDB1

A:Molecule type: mRNA

A:Residues: 1-4 <RES>

A:Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:9601923

C:Genetics:

A:Gene: NF2

Query Match

Best Local Similarity 26.1%; Score 6; DB 2; Length 4;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ei 2

Db 3 EM 4

RESULT 17

PT0696

T-cell receptor beta chain V-D-J region (100-2N) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0612; PT0635; PT0692; PT0552; PT0696
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0635
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE3>
A:Experimental source: newborn thymus, strain BALB/c, 100-2N
A:Accession: PT0612
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AD
A:Accession: PT0692
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE4>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1M
A:Accession: PT0552
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE5>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1CI
A:Accession: PT0696
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE6>
A:Experimental source: newborn thymus, strain BALB/c, 135-1AA
C:Keywords: T cell receptor

Query Match 26.1%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 4 D 4

RESULT 18
PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0607
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE1>
A:Experimental source: newborn thymus, strain BALB/c, 120-2J
A:Accession: PT0674
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A:Accession: PT0678
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE3>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A:Accession: PT0570
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE4>
A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A:Accession: PT0711
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE5>
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C:Keywords: T cell receptor

Query Match 26.1%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 4 D 4

RESULT 19
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C:Accession: A60521
R:Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal
A:Reference number: A60521; MUID:90227907
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
C:Superfamily: phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F.3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status expe

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 e1 2
|
Db 1 Q1 2

RESULT 20
C23751
spinal cord peptide SCP-6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C:Accession: C23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425
A:Accession: C23751
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <HSI>
C:Superfamily: unassigned animal peptides

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|

Db 1 D 1

RESULT 21

A26830
mitosis inhibiting peptide - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A26830
R:Reichelt, K.; Eljjo, K.; Edmison, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A:Reference number: A26830; MUID:87296602
A:Accession: A26830
A:Molecule type: protein
A:Residues: 1-5 <REI>
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 d 4
Db 3 D 3

RESULT 22

B37325
pap fibinrial regulatory protein papi - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C:Accession: B37325
R:Bratzen, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
J. Bacteriol. 173, 1789-1800, 1991
A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex
A:Reference number: A37325; MUID:91154136
A:Accession: B37325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <BRA>
A:Cross-references: GB:M63747

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 e l l 3
Db 3 EYM 5

RESULT 23

A32014
tram protein - Escherichia coli plasmid R100 (fragment)
C:Species: Escherichia coli
C:Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
C:Accession: A32014
R:Inamoto, S.; Yoshioaka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A:Title: Identification and characterization of the products from the traJ and traY gene
A:Reference number: A32014; MUID:88227859
A:Accession: A32014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <INA>
C:Genetics:
A:Genome: plasmid
C:Keywords: DNA binding

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 d 4
Db 3 D 3

RESULT 24

B60274
major protein antigen MP732 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: B60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the cult
A:Reference number: A60274; MUID:91099989
A:Accession: B60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 d 4
Db 1 D 1

RESULT 25

D60274
major protein antigen MP746 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: D60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the cult
A:Reference number: A60274; MUID:91099989
A:Accession: D60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 d 4
Db 2 D 2

RESULT 26

S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (frag
N:Alternate names: xylanase
C:Species: Streptomyces sp.
A:Variety: Chainia sp. NCL 82.5.1
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S70615
R:Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A:Title: Structural environment of an essential cysteine residue of xylanase from Cha
A:Reference number: S70615; MUID:96265041

A:Accession: S70615
A:Molecule type: protein
A:Residues: 1-5 <RAO>
A:Experimental source: Chaetnia sp. strain NCL 82.5.1
A:Note: the source is designated as Chaetnia sp.
C:Function: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A:Description: fermentation of hemicellulose into ethanol
C:Keywords: glycosidase; hydrolase

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
5 D 5

RESULT 27
T14908

hypothetical protein - parsley
C:Species: Petroselinum crispum (parsley)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T14908
R:Kirchner, S.; Ledger, S.; Hayashi, H.; Weishaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A:Title: CPRFA, a novel plant bzp protein of the CPRF family: comparative analysis of
A:Reference number: Z18261; MUID:98265918
A:Accession: T14908
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5 <KIR>
A:Cross-references: EMBL:Y10809; NID:93336901; PDB:CAA71767.1; PID:93336902
A:Experimental source: Hamburger Schmitt

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 11d 5
1 MVS 4

RESULT 28
P00689

Photosystem I 10.4k H1 chain - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C:Accession: P00689
R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
Plant Physiol. 102, 1253-1267, 1993
A:Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal are
A:Reference number: P00689; MUID:94105345
A:Accession: P00689
A:Molecule type: protein
A:Residues: 1-5 <OBO>
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
4 D 4

RESULT 29

A44692
Fulicin - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C:Accession: A44692

R:Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.;
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated fro
A:Reference number: A44692; MUID:91315471
A:Accession: A44692

A:Molecule type: protein
A:Residues: 1-5 <OHT>
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F:2/Modified site: D-asparagine (Asn) #status experimental
F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 e1 3
3 EFV 5

RESULT 30
PT0267

Ig heavy chain CRD3 region (clone 3-94A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0267
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0267
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
5 D 5

RESULT 31
PT0281

Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0281
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 1 D 1

RESULT 32

PT0308
Ig heavy chain CDR3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 393-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 1 D 1

RESULT 33

PT0596
T-cell receptor beta chain V-D-J region (100-2AE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0596; PT0614
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0596
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1H
C:Keywords: T-cell receptor

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 4 D 4

RESULT 34

PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0513; PT0606
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601

A:Accession: PT0513
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>

A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A:Accession: PT0606
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C:Keywords: T-cell receptor

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 4 D 4

RESULT 35

PT0600
T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0600
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0600
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
|
Db 4 D 4

Search completed: June 10, 2002, 06:37:52
Job time: 75 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:37:57 ; Search time 11.71 Seconds

(without alignments)
16.533 Million cell updates/sec

Title: 09-251073

Perfect score: 23

Sequence: 1 e1ldv 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwisProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34.8	8	34.8	1 LUXE_VIBRI	P24272 vibrio fusc
2	34.8	8	34.8	2 UC22_MAIZE	P80628 zea mays (m
3	30.4	7	30.4	5 RE1_LITRU	P82070 litorea rub
4	26.1	6	26.1	1 ACHL_ACHRU	P35904 achetina fu
5	26.1	6	26.1	4 OCPI_OCTMI	P38648 octopus min
6	26.1	6	26.1	1 OCPI_OCTMI	P38648 octopus min
7	26.1	6	26.1	5 B10A_CITFR	P13071 citrobacter
8	26.1	6	26.1	1 TRM3_ECOLI	P13973 escherichia
9	26.1	6	26.1	5 UXA4_CHLTR	P38005 chlamydia t
10	21.7	5	21.7	4 EOST_HUMAN	P02731 homo sapien
11	21.7	5	21.7	1 E104_LITRU	P82100 litorea rub
12	21.7	5	21.7	5 RE21_LITRU	P82071 litorea rub
13	21.7	5	21.7	1 RE31_LITRU	P82072 litorea rub
14	17.4	4	17.4	4 FAR3_HIRME	P42565 hirudo medi
15	17.4	4	17.4	1 FLRF_HIRME	P42565 hirudo medi
16	17.4	4	17.4	4 FLRN_ANTEL	P38707 antioleura
17	17.4	4	17.4	4 FYRI_ANTEL	P38706 antioleura
18	17.4	4	17.4	4 RM01_YEAST	P36515 saccharomyc
19	17.4	4	17.4	5 E103_CARMA	P81817 carinus ma
20	17.4	4	17.4	5 E103_LITRU	P82099 litorea rub
21	17.4	4	17.4	5 PAPT_PERAM	P81857 attiposchi
22	17.4	4	17.4	5 PAPT_PERAM	P81857 attiposchi
23	17.4	4	17.4	5 PSK_DAUCA	P38261 daucus caro
24	17.4	4	17.4	5 RE32_LITRU	P82073 litorea rub
25	17.4	4	17.4	5 TPIS_CANFA	P44714 canis fami
26	17.4	4	17.4	5 UF01_MOUSE	P11515 mus muscul
27	8.7	2	8.7	3 THYL_PIG	P11515 sus scrofa
28	8.7	2	8.7	4 DCM1_PSECH	P19916 pseudomonas
29	8.7	2	8.7	4 DCM5_PSECH	P19918 pseudomonas
30	8.7	2	8.7	4 FAR4_HIRME	P42563 hirudo medi
31	8.7	2	8.7	4 FMRF_MACNI	P01162 macrocallis
32	8.7	2	8.7	5 B10B_CITFR	P12997 citrobacter
33	8.7	2	8.7	5 BPP7_BOTIN	P30425 botnops in

34	1	4.3	3	1	GRM_HUMAN	P01157 homo sapien
35	1	4.3	4	1	FEKA_ANTEL	P38705 antioleura
36	1	4.3	4	1	TUFT_HUMAN	P01858 homo sapien
37	0	0.0	5	1	PAPT_PARMA	P81864 parachlirus
38	0	0.0	5	1	SUGA_ACHDO	P19991 acheta dome

ALIGNMENTS

RESULT	ID	LUXE_VIBRI	STANDARD	PRT	3 AA
AC	P24272	01-MAR-1992 (Rel. 21, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)				
DE	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (acyl-protein synthetase) (Fragment).				
GN	LUXE.				
OS	Vibrio fischeri.				
OC	Bacteria; Proteobacteria; gamma subphylum: Vibrionaceae; Vibrio.				
OX	NCBI_TaxID=668;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91072226; PubMed=2254256;				
RA	Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;				
RT	"A new Vibrio fischeri lux gene precedes a bidirectional termination site for the lux operon."				
RL	J. Bacteriol. 172:6797-6802(1990).				
CC	-1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.				
CC	IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.				
CC	-1- CATALYTIC ACTIVITY: ATP + 14n acid + protein -> AMP + diphosphate + an acyl-protein thioester.				
CC	-1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE COMPLEX.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: M62812; -; NOT_ANNOTATED_CDS.				
KM	luminescence; ligase.				
NC	NCBI_TaxID=668;				
SO	SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;				
QY	2	1ld 4			
DB	1	IKD 3			
RESULT	2				
UC22_MAIZE	STANDARD;	PRT;	5 AA.		
AC	P80628;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Unknown protein from 2D-page of etiolated coleoptille (Spot 474) (Fragment).				
DE	Zea mays (Maize).				
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				

Query Match 34.8%; Score 8; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoidae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Toulzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 KDa.
 DR Maize-2DPAGE; P80628; COLEOPTILE.
 DR MaizeDB; 123954; "
 FT NON_TER 1 1
 FT 5 5
 SQ SEQUENCE 5 AA: 654 MW: 72CB199C0300000 CRC64;

Query Match 34.8%; Score 8; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ei 2
 DB 4 EV 5

RESULT 3
 REEL_LITRU STANDARD; PRT; 5 AA.
 AC P82070;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OX Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=598; METHOD=FAB.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA: 598 MW: 60D9C9CAB2A00000 CRC64;

Query Match 30.4%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 Id 4
 DB 1 VD 2

RESULT 4
 ACCH_ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatin-I.
 OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=FERUSSAC; TISSUE=Ganglion;
 RX MEDLINE=92273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Di P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue."
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION, TISSUE=Heart atrium;
 RC STRAIN=FERUSSAC; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function."
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue."
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE. INCREASES THE IMPULSE FREQUENCY
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 CC PIR: A32480; A32480.
 DR Hormone; D-amino acid.
 KW MOD_RES 2
 FT MOD_RES 2
 SQ SEQUENCE 4 AA: 408 MW: 6AADD9C810000000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
 DB 4 D 4

RESULT 5
 OCPL_OCTMI STANDARD; PRT; 4 AA.
 AC P58648;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocpl-1/Ocp-2.
 OS Octopus minor (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; coleoidea; Octopoda;
 CC Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor."

```

RL Peptides 21:623-630(2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KM Hormone: D-amino acid.
FT MOD_RES 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 26.18; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
DB 4 D 4

RESULT 6
OCP2_OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
ON NCBI_TaxID=89766;
RX [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX PubMed-10876044;
RA Iwakoshi E., Minakata H.;
RT Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.
RL Peptides 21:623-630(2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KM Hormone: D-amino acid.
FT MOD_RES 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 26.18; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
DB 4 D 4

RESULT 7
BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-7-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA
OS Citrobacter freundii.

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OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69006280; PubMed=2971595;
RA Shuhan D., Campbell A.;
RT "transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RT Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: BIOTIN BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; M21922; ; NOT ANNOTATED CDS.
DR InterPro; IPR000954; AminoTran_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KM Biotin biosynthesis; Transferase; Aminotransferase;
KM Pyridoxal phosphate.
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1BA6F00000 CRC64;

Query Match 26.18; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
DB 4 D 4

RESULT 8
TRM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trm protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Iinamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the trm
RT and trm genes of plasmid R100."
RL J. Bacteriol. 170:2749-2757(1988).
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC -----
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DR EMBL; M20941.1; NOT_ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
SO SEQUENCE 5 AA: 634 MW; 6B1B1AA443500000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
Db 3 d 3

RESULT 9
ID UX44.CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCB1_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=12/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Viretton E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 Kda.
DR Sjena-2DPAGE; P38005; -
FT NON_TER 5
SQ SEQUENCE 5 AA: 474 MW; 75BAA865AA800000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 d 4
Db 4 d 4

RESULT 10
ID E051.HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilic peptidase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; Pubmed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of

RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR PIR; A03190; ETHQL.
FT VARIANT 1
SO SEQUENCE 4 AA: 390 MW; 6B05862A0000000 CRC64;

Query Match 21.7%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
Db 4 E 4

RESULT 11
ID E104.LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Electrin 4.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
NCB1_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litorea rubella. Comparison with the skin peptides from Litorea
RT rubella";
RL Aust. J. Chem. 52:0-0(1999).
CC -1- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA: 616 MW; 61F2D1A059A00000 CRC64;

Query Match 21.7%; Score 5; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 Idv 5
Db 2 ITV 4

RESULT 12
ID RE21.LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Rubellidin 2.1.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
NCB1_TaxID=104895;
RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RT Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=626; METHOD=FAB.
 CC Amphibian skin.
 KW MOD_RES 5
 SO SEQUENCE 5 AA: 626 MW: 6DD9C9CB10300000 CRC64;

Query Match 21.7%; Score 5; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
 Db 2 E 2

RESULT 13
 RE31_LITRU
 ID RE31_LITRU STANDARD; PRT; 5 AA.
 AC P82072;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 NC NCB1_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RT Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=635; METHOD=FAB.
 CC Amphibian skin; Amidation.
 KW MOD_RES 5
 SO SEQUENCE 5 AA: 656 MW: 71A9C9CB10300000 CRC64;

Query Match 21.7%; Score 5; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
 Db 2 E 2

RESULT 14
 FAR3_HIRME
 ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.

OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Atychobdellida; Hirudiniformes; Hirudinae; Hirudo.
 OX NCB1_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech";
 RL Peptides 12:897-908(1991).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 4
 SO SEQUENCE 4 AA: 598 MW: 69D4073B30000000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
 Db 2 L 2

RESULT 15
 FLRF_HIRME
 ID FLRF_HIRME STANDARD; PRT; 4 AA.
 AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FLRFamide.
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Atychobdellida; Hirudiniformes; Hirudinae; Hirudo.
 NC NCB1_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-H.medicalinalis;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech";
 RL Peptides 12:897-908(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-H.trivolvis; TISSUE-Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolvis";
 RL Peptides 15:31-36(1994).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 4
 SO SEQUENCE 4 AA: 582 MW: 69D40729A0000000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
 Db 2 L 2

RESULT 16
 FLRN_ANTEL
 ID FLRN_ANTEL STANDARD; PRT; 4 AA.

AC P58707;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Antho-Rhamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
 OC Nynanthae; Actiniidae; Anthopleura.
 RN NCBI_Taxid=6110;
 [1]
 RP SEQUENCE AND MASS-SPECTROMETRY.
 RA PubMed=1973541;
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
 RA Reinscheid R.K., Notthacker H.-P., Staley A.L.;
 RT "Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-Rhamide), a sea
 RT anemone neuropeptide containing an unusual amino-terminal blocking
 RT group.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron-specific.
 CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAH.
 KM Neuropeptide; Amidation.
 FT MOD_RES 1 4 L-3-PHENYLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA: 549 MW: 64540729A0000000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 1 3
 Db 2 1 2

RESULT 17
 FYRI_AMEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Antho-Rhamide I [Contains: Antho-Rhamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
 OC Nynanthae; Actiniidae; Anthopleura.
 RN NCBI_Taxid=6110;
 [1]
 RP SEQUENCE.
 RA PubMed=1821096;
 RA Notthacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 RT biologically active L-3-phenylacetyl-Tyr-Arg-Ile-NH2 and its
 RT des-phenylacetyl fragment Tyr-Arg-Ile-NH2.";
 RL Peptides 12:1165-1173(1991).
 RN [2]
 RP FUNCTION.
 RX PubMed=8397415;
 RX McFarlane I.D., Hudman D., Notthacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-Kamide and Antho-Rhamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron-specific.
 KM Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD_RES 1 1 L-3-PHENYLACTYL.

FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA: 598 MW: 60441B59A0000000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1 2
 Db 4 1 4

RESULT 18
 RM01_YEAST STANDARD; PRT; 4 AA.
 ID RM01_YEAST
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN MRPL1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 RN NCBI_Taxid=4932;
 [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria.";
 RL FEBS Lett. 284:51-56(1991).
 DR PIR: S17255; S17255.
 DR SGD: L0002681; MRPL1.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA: 402 MW: 7771B2D5D0000000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 5
 Db 2 2

RESULT 19
 AL14_CARMA STANDARD; PRT; 5 AA.
 ID AL14_CARMA
 AC P81817;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eudrachyura; Portunodea; Portunidae; Carcinus.
 RN NCBI_Taxid=6759;
 [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RA MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997)
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -1- SIMILARITY: BELONGS TO THE ALMATOSTATIN FAMILY.
KM Neuropeptide: Amidation; Multigene family.
FT MOD_RES 5 AA: 586 MW; 672879D5AB300000 CRC64;
SQ SEQUENCE 5 AA: 586 MW; 672879D5AB300000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
DB 5 L 5

RESULT 20
E103_LITRU STANDARD; PRT; 5 AA.
AC P82059;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP TISSUE-Skin secretion;
RA Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
RT Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RL rubella.";
RL Aust. J. Chem. 52:0-0(1999).
CC -1- SUBCELLULAR LOCATION: SECRETED.
KM Amphibian skin: Amidation.
FT MOD_RES 5 AA: 630 MW; 668761F2C9A00000 CRC64;
SQ SEQUENCE 5 AA: 630 MW; 668761F2C9A00000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 V 5
DB 2 V 2

RESULT 21
FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRamide-like neuropeptide RYRF-amide.
OS Artloposchia triangulata.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabdiphora; Sericata; Tricladida; Terricola; Geoplanidae;
OC Archidendys.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE. AND SYNTHESIS.
RA MEDLINE=94211927; Pubmed=7909164;
RA Maulé A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYRFamide: a turbellarian FMRamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KM Neuropeptide: Amidation.

FT MOD_RES 5 AA: 754 MW; 69D4004B44600000 CRC64;
SQ SEQUENCE 5 AA: 754 MW; 69D4004B44600000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1 2
DB 3 I 3

RESULT 22
PRTC_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach).
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; Pubmed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; Pubmed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; Pubmed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; Pubmed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PTR: A01644; HOROHA.
DR PTR: A60411; A60411.
KM Neuropeptide.
SQ SEQUENCE 5 AA: 649 MW; 71B7673B44600000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 1 3
1
Db 3 L 3

RESULT 23
PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cv. US-Harumakigosun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kamada H., Sakagami Y.;
RT "A secreted peptide growth factor, phytosulfokine, acting as a
RT stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC -1- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PFM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1 2
1
Db 2 I 2

RESULT 24
RE32_LITRU STANDARD; PRT; 5 AA.
ID RE32_LITRU
AC P82073;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";

RL Aust. J. Chem. 52:0-0(1999).
CC -1- FUNCTION: SHOW NEUTROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 v 5
1
Db 1 V 1

RESULT 25
TPIS_CANFA STANDARD; PRT; 5 AA.
ID TPIS_CANFA
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN TP1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceroone
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR Interpro: IPR000652; Trioseph_isomerase.
DR PROSITE: PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_TER 3 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 v 5
1
Db 2 V 2

RESULT 26
UF01_MOUSE STANDARD; PRT; 5 AA.
ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCRT_TaxID=10090;
 RN [1]
 RC SEQUENCE.
 RX TISSUE=Fltproblast; PubMed=7523108;
 RA MEDLINE=95009907; PubMed=7523108;
 RT Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1 2
 DB 2 1 2

RESULT 27
 ID THYL_PIG STANDARD; PRT; 3 AA.
 AC P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thyloliberin (Thyrotropin releasing hormone) (TRH) (Protrelin).
 OS Sus scrofa (Pig).
 OS Ovis aries (Sheep).
 OS Bombina orientalis (Oriental fire-bellied toad), and
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823, 9940, 8346, 8316;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Pig; TISSUE=Hypothalamus;
 RX MEDLINE=70136150; PubMed=484938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 "Structure of porcine thyrotropin releasing hormone.";
 RT Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SYNTHESIS.
 RC SPECIES=Pig;
 RX MEDLINE=70039904; PubMed=4982117;
 RA Bolter J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 "The identity of chemical and hormonal properties of the thyrotropin
 releasing hormone and pyroglutamyl-histidyl-proline amide.";
 RT Biochem. Biophys. Res. Commun. 37:705-710(1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Hypothalamus;
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
 RA Ward D.N.;
 "The elucidation of the primary structure of the hypothalamic thyroid
 stimulating hormone releasing factor of ovine origin by means of mass
 spectrometry.";
 RT Org. Mass Spectrom. 5:221-228(1971).
 RN [4]
 RP SYNTHESIS.
 RC SPECIES=Sheep;
 RX MEDLINE=70163386; PubMed=4985794;
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RA Guillemin R.;
 "Characterization of ovine hypothalamic hypophysiotropic
 TSH-releasing factor.";
 RT Nature 226:321-325(1970).
 RN [5]

RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RN [6]
 RP SEQUENCE.
 RC SPECIES=N.viridescens;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 viridescens) brain in vitro. Isolation and characterization of
 thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
 DR PIR: A01415; RHPCR.
 DR PIR: A93750; RSHST.
 DR PIR: A90919; RHPTDQ.
 DR PIR: A92971; A92971.
 KW Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 3 3 AMIDATION.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
 DB 1 Q 1

RESULT 28
 ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (fragment).
 OS Pseudomonas carboxydohydrogenans.
 CC Bacteria; Proteobacteria.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Krait M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrogenic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: P10140; P10140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
 DB 1 M 1

RESULT 29
DCMS_PSECH STANDARD: PRT: 4 AA.
AC P19918:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (Fragment).
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT cardoxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: P10146; P10146.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA: 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 1 3
Db 1 M 1

RESULT 30
FAR4_HIRME STANDARD: PRT: 4 AA.
AC P42563:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA: 616 MW; 69D4068B30000000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy * 3 1 3
Db 2 M 2

RESULT 31
FMRF_MACNI STANDARD: PRT: 4 AA.
AC P01162:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrococlistia nimosa (Sun-ray clam).
OS Nereis virens (Sandworm).
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Veneroida;
OC Veneroida; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC SPECIES=M.nimosa; TISSUE=Cerebral pedal, and visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RC SPECIES=M.nimosa; TISSUE=Ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
RT from the central ganglia of a bivalve mollusc.";
RL Prep. Biochem. 7:261-281(1977).
RN [3]
RP SEQUENCE.
RC SPECIES=N.virens;
RX MEDLINE=90259866; PubMed=2342992;
RA Krajnak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL Peptides 11:75-77(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [5]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
CC ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CC CARDIAC CONTRACTION.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A01426; ECKN.
DR PIR: A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA: 600 MW; 69D4069A00000000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 1 3
Db 2 M 2

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RESULT 32
BIOL_CITFR STANDARD; PRT: 5 AA.
ID BIOL_CITFR
AC P12997;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN BIOL.
OS Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OC Citrobacter.
NCBI_TaxID=346;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: Dethiobiotin + sulfur -> biotin.
CC -1- PATHWAY: Biotin biosynthesis; last step.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPIC ACID SYNTHETASES
CC FAMILY.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: M21922; -; NOT_ANNOTATED_CDS.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER
SQ SEQUENCE 5 AA: 532 MW: 75A5B1EDD6F0000 CRC64:

Query Match 8.7%; Score 2; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
DB 1 M 1

RESULT 33
BPP7_BOTIN STANDARD; PRT: 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide 55,2 (5a) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Quelana jararaca).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RX MEDLINE=90351557; PubMed=2386615;
RA Chitra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF

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CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1
SQ SEQUENCE 5 AA: 629 MW: 776DC37328B00000 CRC64:

Query Match 8.7%; Score 2; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
DB 1 Q 1

RESULT 34
GRMW_HUMAN STANDARD; PRT: 3 AA.
ID GRMW_HUMAN
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR PIR: A01421; GRHU.
SQ SEQUENCE 3 AA: 340 MW: 6331E81000000000 CRC64:

Query Match 4.3%; Score 1; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
DB 3 K 3

RESULT 35
FFKA_AMEL STANDARD; PRT: 4 AA.
ID FFKA_AMEL
AC P58705;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Antho-Kamide.
OS Anthopleura elegantissima (Sea anemone).
OS Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymphaeae; Actinellidae; Anthopleura.
NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L., Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenylalanyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RT novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;

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RT "The expansion behaviour of sea anemones may be coordinated by two
 RL inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -I- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: Neuron-specific.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 L-3-PHENYLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 4.3%; Score 1; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 e 1
 :
 Db 3 K 3

Search completed: June 10, 2002, 06:41:57
 Job time: 240 sec

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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:37:17 ; Search time 25.17 Seconds
(without alignments)
34.365 Million cell updates/sec

Title: 09-251073

Perfect score: 23

Sequence: 1 eildv 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

1: SP-ARCHEA:19:*
2: SP-BACTERIA:*
3: SP-FUNGI:*
4: SP-HUMAN:*
5: SP-INVERTEBRATE:*
6: SP-MAMMAL:*
7: SP-MHC:*
8: SP-ORGANELLE:*
9: SP-PHAGE:*
10: SP-PLANT:*
11: SP-RODENT:*
12: SP-VIRUS:*
13: SP-VERTEBRATE:*
14: SP-UNCATEGORIZED:*
15: SP-VIRUS:*
16: SP-BACTERIAP:*
17: SP-ARCHEAP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	30.4	4	11 Q08433	Q08433 ratu
2	7	30.4	5	13 P82070	P82070 litoria
3	6	26.1	5	13 P83073	P83073 bacillus
4	5	21.7	5	13 P82071	P82071 litoria
5	5	21.7	5	13 P82072	P82072 litoria
6	5	21.7	5	13 P82100	P82100 litoria
7	4	17.4	5	13 P82073	P82073 litoria
8	4	17.4	5	13 P82099	P82099 litoria
9	2	8.7	5	10 Q99007	Q99007 hordeum

ALIGNMENTS

RESULT 1
Q08433

ID Q08433 PRELIMINARY: PRT: 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-JAN-1999 (TREMUREL. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashimata S., Koike O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat." 177:1161-1164(1991).
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR
CC -1- BETA-D-GLUCURONOSIDE. MICROsome.
CC -1- SUBCELLULAR LOCATION: MICROsome.
DR EMBL; S38636; AAB19259.1; -;
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA: 473 MW: 633732CA20000000 CRC64;

Query Match 30.4%; Score 7; DB 11; Length 4;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 11.3
Db 2 VL 3

RESULT 2
ID P82070 PRELIMINARY: PRT: 5 AA.
AC P82070;
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowle J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
Litoria rubella: the skin peptide profile as a probe for the study
of evolutionary trends of amphibians." 49:955-963(1996).
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA: 598 MW: 6DD9C9CAB2A00000 CRC64;

Query Match 30.4%; Score 7; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 1d 4
 Db 1 VD 2

RESULT 3
 ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE 88 KDA PROTEIN (FRAGMENT).
 OS Bacillus cereus.
 OC Bacillus: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER
 SO SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 26.1%; Score 6; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 d 4
 Db 3 D 3

RESULT 4
 ID P82071 PRELIMINARY; PRT; 5 AA.
 AC P82071;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE RUBELLIDIN 2.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 ANTIIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=626; METHOD=FAB.
 KW Amphibian skin.
 SO SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 21.7%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 e 1
 Db 1 e 1

Db 2 E 2

RESULT 5
 ID P82072 PRELIMINARY; PRT; 5 AA.
 AC P82072;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE RUBELLIDIN 3.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 ANTIIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=655; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES
 SO SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 21.7%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 e 1
 Db 2 E 2

RESULT 6
 ID P82100 PRELIMINARY; PRT; 5 AA.
 AC P82100;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ELECTRIN 4.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 52:0-0(1999).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 ANTIIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=655; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES
 SO SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 21.7%; Score 5; DB 13; Length 5;
 Best Local Similarity 33.3%; Pred. No. 5.6e+05;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 Adv 5
DB 2 ITV 4

RESULT 7
P82073 PRELIMINARY; PRT: 5 AA.
AC P82073;
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DE 01-MAY-2000 (TREMUREL. 13, Last annotation update)
OS RUBELLIDIN 3.2.
OC Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KM Amphibian skin.
SO SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 17.4%; Score 4; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 v 5
DB 1 v 1

RESULT 8
P82099 PRELIMINARY; PRT: 5 AA.
AC P82099;
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DE 01-MAY-2000 (TREMUREL. 13, Last annotation update)
OS ELECTRIN 3.
OC Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KM Amphibian skin; Amidation.
FT MOD RES 5
SO SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 17.4%; Score 4; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 v 5

DB 2 v 2

RESULT 9
O99007 PRELIMINARY; PRT: 5 AA.
AC O99007;
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DE 01-NOV-1998 (TREMUREL. 08, Last annotation update)
OS ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
CN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
CC EMBL: X54643; CAA38455.1;
KM Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON-TER 5
SO SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 8.7%; Score 2; DB 10; Length 5;
Best Local Similarity 0.0%; Pred. No. 5.6e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 1 3
DB 1 M 1

Search completed: June 10, 2002, 06:41:24
Job time: 247 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:36:38 ; Search time 24.27 Seconds
(without alignments)
22.883 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eldav 5

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 21101

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_032802.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	5	17 AAR95719	Alpha-4beta-1 inte
2	23	100.0	5	18 AAW25192	LDV-peptide capabl
3	23	100.0	5	19 AAW46318	Peptide recognisad
4	23	100.0	5	20 AAY03855	Integrin ligand d1
5	23	100.0	5	21 AAY80488	Cell adhesion pept
6	23	100.0	5	21 AAT77442	Fibronectin CSI-de
7	23	100.0	5	21 AAT69619	VLA-4 inhibitor pe
8	23	100.0	5	22 AAB73465	Fibronectin VLA-4
9	23	100.0	5	22 AAB91966	Fibronectin fragme
10	23	100.0	5	22 AAB50876	Integrin recogniti
11	23	100.0	5	22 AAB59135	Peptide #3 recogni

12	19	82.6	5	17 AAR9752	Cyclic peptide inh
13	18	78.3	4	21 AAT77441	Fibronectin CSI-de
14	18	78.3	4	21 AAY51252	Cyclizing peptide
15	18	78.3	5	16 AAW01724	Inhibitor of fibro
16	18	78.3	5	18 AAW45730	Precursor peptide
17	18	78.3	5	21 AAT77428	Fibronectin CSI pe
18	18	78.3	5	21 AAT77431	Fibronectin CSI pe
19	17	73.9	5	17 AAR2849	Cell adhesion modu
20	16	69.6	5	17 AAR95707	Alpha-4beta-1 inte
21	16	69.6	5	17 AAR95716	Alpha-4beta-1 inte
22	16	69.6	5	17 AAR95717	Alpha-4beta-1 inte
23	16	69.6	5	17 AAR9748	Cyclic peptide inh
24	16	69.6	5	18 AAW45731	Precursor peptide
25	16	69.6	5	20 AAY30308	Angiotensin deriv
26	14	60.9	3	16 AAR82907	Non-RGD, non-YISGR
27	14	60.9	3	18 AAW25187	LDV-peptide capabl
28	14	60.9	3	21 AAB01568	Cell binding domai
29	14	60.9	3	22 AAB91984	Fibronectin fragme
30	14	60.9	4	10 AAB91609	Motif useful in to
31	14	60.9	4	16 AAW01711	Inhibitor of fibro
32	14	60.9	4	16 AAR66483	Sodium channel gen
33	14	60.9	4	17 AAR95728	Alpha-4beta-1 inte
34	14	60.9	4	17 AAR95731	Alpha-4beta-1 inte
35	14	60.9	4	17 AAR95726	Alpha-4beta-1 inte
36	14	60.9	4	17 AAR95704	Alpha-4beta-1 inte
37	14	60.9	4	17 AAR95714	Alpha-4beta-1 inte
38	14	60.9	4	19 AAW55750	Immunisation motif
39	14	60.9	4	21 AAG80707	Fibronectin-derive
40	14	60.9	4	21 AAT77420	Fibronectin CSI pe
41	14	60.9	4	22 AAB81415	Integrin alpha4bet
42	14	60.9	4	22 AAB59922	Human leptin fragm
43	14	60.9	5	6 AAF50562	Sequence of peptid
44	14	60.9	5	14 AAR33614	Pseudopeptide rhyt
45	14	60.9	5	14 AAR31940	In vivo tumour bin
46	14	60.9	5	15 AAR95983	Peptide signal seq
47	14	60.9	5	16 AAW01722	Inhibitor of fibro
48	14	60.9	5	16 AAW01718	Inhibitor of fibro
49	14	60.9	5	17 AAR95708	Alpha-4beta-1 inte
50	14	60.9	5	17 AAR91725	NAP subsequence.
51	14	60.9	5	17 AAR99756	Cyclic peptide inh
52	14	60.9	5	17 AAR99757	Cyclic peptide inh
53	14	60.9	5	17 AAW00406	Interleukin-6 anta
54	14	60.9	5	18 AAW02055	Peptide used to pr
55	14	60.9	5	18 AAW25189	LDV-peptide capabl
56	14	60.9	5	18 AAW25191	Endo-beta1,4-gluca
57	14	60.9	5	19 AAW46813	Nematode extracted
58	14	60.9	5	20 AAY30444	Inhibitor peptide
59	14	60.9	5	20 AAW88079	NAP domain fragmen
60	14	60.9	5	21 AAB15329	Peptide derived fr
61	14	60.9	5	21 AAB08242	Peptide motif from
62	14	60.9	5	21 AAY93436	Peptide cyclo-(Leu
63	14	60.9	5	21 AAY82724	N. dentriticiflans a
64	14	60.9	5	21 AAY87605	Cell adhesion pept
65	14	60.9	5	21 AAY80491	Fibronectin CSI pe
66	14	60.9	5	21 AAT77427	Fibronectin CSI pe
67	14	60.9	5	21 AAY69620	VLA-4 inhibitor pe
68	14	60.9	5	22 AAB73466	Fibronectin VLA-4
69	14	60.9	5	22 AAB91985	Fibronectin fragme
70	13	56.5	4	21 AAY94573	Peptide based endo
71	13	56.5	4	21 AAY43756	Amino acid sequenc
72	13	56.5	4	22 AAB30758	Peptide which is u
73	13	56.5	5	13 AAR31316	Alpha-substituted
74	13	56.5	5	13 AAR29448	Endothelin antagou
75	13	56.5	5	13 AAR29449	Endothelin antagou
76	13	56.5	5	13 AAR29450	Endothelin antagou
77	13	56.5	5	13 AAR29451	Endothelin antagou
78	13	56.5	5	13 AAR29452	Endothelin antagou
79	13	56.5	5	15 AAR54601	Cholecyctokinin an
80	13	56.5	5	15 AAR54602	Cholecyctokinin an
81	13	56.5	5	15 AAR54603	Cholecyctokinin an
82	13	56.5	5	15 AAR54604	Cholecyctokinin an
83	13	56.5	5	15 AAR54605	Cholecyctokinin an
84	13	56.5	5	15 AAR69220	Endothelin C-termi

85	13	56.5	5	15	AAR69221	Endothelin C-term1
86	13	56.5	5	15	AAR69222	Endothelin C-term1
87	13	56.5	5	15	AAR69223	Endothelin C-term1
88	13	56.5	5	15	AAR69224	Endothelin C-term1
89	13	56.5	5	15	AAR69236	Endothelin C-term1
90	13	56.5	5	16	AAW01727	Inhibitor of fibro
91	13	56.5	5	19	AAW69701	HGAR and MGAR pept
92	13	56.5	5	19	AAW65871	Osteopontin recepto
93	13	56.5	5	19	AAW63604	Osteopontin derivate
94	13	56.5	5	21	AAW28654	Chemotactic peptid
95	13	56.5	5	21	AAW28658	Chemotactic peptid
96	13	56.5	5	21	AAW28669	Chemotactic peptid
97	13	56.5	5	21	AAW28670	Chemotactic peptid
98	13	56.5	5	21	AAW83335	D region motif of
99	13	56.5	5	21	AAW77432	Fibronectin CSI pe
100	13	56.5	5	21	AAW69538	Bioactive peptide

ALIGNMENTS

RESULT 1

AAW5719 standard; peptide: 5 AA.

AAW5719;

04-DEC-1996 (first entry)

Alpha-4beta-1 integrin binding inhibitory peptide 16.

VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
inhibitor; binding; white blood cell; migration; capillary wall;
tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
CSI; CS5; HI; LDV; active site.

Synthetic.

OS	XX	Key	Location/Qualifiers
PH	XX	Modified-site	5 /note="Val-NH2"

US5510332-A.

23-APR-1996.

07-JUL-1994; 94US-0271830.

07-JUL-1994; 94US-0271830.

(TEXA-) TEXAS BIOTECHNOLOGY CORP.

Beck PJ, Kogan TP, Ren K, Vanderslice P;

WPI; 1996-221274/22.

New peptide(s) based on the LDV domain of fibronectin - used for
inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
fibronectin or invasion

Disclosure; Column 21-22; 35pp; English.

VCAM-1 is protein found on the
surface of endothelial cells that line the interior wall of capillaries.
VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
VLA-4 for very late antigen-4), a heterodimeric protein present on the
surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
white blood cells to adhere to the capillary wall in areas where the
tissue surrounding the capillary has been infected or damaged. Sometimes
this white blood cell migration can become uncontrolled, with white
blood cells flooding to the scene, causing widespread tissue damage.
Cpds. capable of blocking this process may be beneficial as therapeutic
agents. IA4B1 also recognises the extracellular matrix glycoprotein

CC fibronectin. Three distinct IA4B1-binding sites have been identified
CC within fibronectin. One site is found in the HepII region and is
CC expressed in all isoforms; two others (CS1 and CS5) are present in the
CC alternatively spliced type III connecting segments. CS1 has the higher
CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC site. Peptides AAR5794-805 are modeled after a portion of the CS1
CC peptide that include the LDV domain presented in such a way by its novel
CC flanking sequence to produce a potent inhibitor of IA4B1 binding.

Sequence 5 AA:

Query Match 100.0%; Score 23; DB 17; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	elldv	5
DB	1	elldv	5

RESULT 2

AAW25192 standard; peptide: 5 AA.

AAW25192;

05-JAN-1998 (first entry)

LDV-peptide capable of binding cell adhesion molecules.

LDV; leucine; aspartic acid; valine; cell adhesion molecule;
binding; bladder irrigation; tumour removal; endoscopic operation;
transurethral resection; cancer; neoplasia.

Synthetic.

OS	XX	DEL9529909-A1.
PN	XX	20-FEB-1997.

15-AUG-1995; 95DE-1029909.

15-AUG-1995; 95DE-1029909.

(PREP) FRESSENIUS AG.

Boehle A.

WPI; 1997-133793/13.

Endoscopic irrigation solns. - contg. peptide(s) that bind to cell

adhesion molecules

Claim 6; Page 8; 8pp; German.

AAW25187-W25192 are peptides containing an LDV sequence or equivalent.

The peptides are capable of binding to cell adhesion molecules and
are used in aqueous irrigation solutions for use during and after

endoscopic operations. Preferred irrigation solutions are
electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more

oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
GRRP, VLR, YIGSR, KQAGDV and/or REDV (given in one letter amino acid

code). The solutions are especially used for irrigating the bladder
during and after tumour removal by transurethral resection. The

peptides protect against recurrence of tumours.

Sequence 5 AA:

Query Match 100.0%; Score 23; DB 18; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
 DB 1 eildv 5

RESULT 3

AAW46318
 ID AAW46318 standard; Protein: 5 AA.

AC AAW46318;

DT 08-MAY-1998 (first entry)

DE Peptide recognised by Integrin alpha4beta1.

XX Fibrinogen; integrin; alpha-IIB-beta3; cell surface receptor;
 KM penton base protein; coat proteins; adenovirus; binding site;
 KM cellular adhesion; extracellular matrix molecule; binding domain;
 KM cell surface binding site; Dispecific molecule; gene therapy.

OS Unidentified.

PN US5712136-A.

PD 27-JAN-1998.

PF 17-APR-1996; 96US-0634060.

PR 08-SEP-1994; 94US-0303162.

XX (GENV-) GENVEC INC.

XX Brough DE, Bruder JT, Kovesdi I, McVey DL, Roelvink PW;
 PI Wickham TJ;

DR MPI; 1998-119984/11.

PT Methods for introducing adenovirus into cells - used for genetic
 XX engineering and gene therapy

PS Claim 27; Column 2; 56pp; English.

CC The present sequence is a linear stretch of amino acids (present in
 CC fibronectin) recognised by the integrin alpha4beta1. Integrins are
 CC cell surface receptors. The penton base protein (one of the coat
 CC proteins) of adenoviruses binds to integrins. The integrins not only
 CC provide a binding site for the adenoviral penton base protein, but also
 CC mediate cellular adhesion to the extracellular matrix molecules. The
 CC specification describes a method of introducing an adenovirus into
 CC a cell in vitro having a particular cell surface binding site. The
 CC adenovirus is contacted with a bispecific molecule comprising a component
 CC that selectively binds a binding domain of the penton base protein of the
 CC adenovirus and a second component that selectively binds the cell surface
 CC binding site. A complex of the adenovirus and the bispecific molecule is
 CC formed, and the cell is contacted with it to allow entry of the
 CC adenovirus into the cell. The methods can be used for research and the
 CC vectors can be used for gene therapy.

SO Sequence 5 AA:

Query Match 100.0%; Score 23; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
 DB 1 eildv 5

RESULT 4

AAV03855

ID AAV03855 standard; peptide; 5 AA.

AC AAV03855;

DT 16-JUN-1999 (first entry)

DE Integrin ligand dissociator (ILD) peptide.

XX Integrin-11gand; dissociator; disaggregation; platelet thrombus; stroke;
 KM fibrinogen; glycoprotein IIB-IIIA; angina; myocardial infarction; bone;
 KM osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
 KM psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
 KM organ transplant rejection; arthritis; ILD.

OS Synthetic.

PN WO9911280-A1.

PD 11-MAR-1999.

PF 03-SEP-1998; 98WO-US18305.

PR 03-SEP-1997; 97US-0057463.

XX (BURN-) BURHAM INST.

XX Hu DD, Smith JW;

DR MPI; 1999-243586/20.

PT Disaggregating a ligand; integrin receptor complex

XX Disclosure; Page 10; 39pp; English.

CC The invention relates to integrin ligand dissociators. Disaggregation of
 CC an existing platelet thrombus in a blood vessel is due to dissociation of
 CC fibrinogen from glycoprotein IIB-IIIA. This dissociation is caused by the
 CC binding of an Integrin-11gand dissociator at ligand binding site I of
 CC glycoprotein IIB-IIIA. The invention provides a method of disaggregating
 CC an existing platelet thrombus in a blood vessel, where the platelet
 CC thrombus may form an occlusion of a blood vessel, in a subject comprises
 CC administering a compound which dissociates fibrinogen bound to a first
 CC site on platelet glycoprotein IIB-IIIA, by binding to a second
 CC interacting site on platelet glycoprotein IIB-IIIA, disaggregating the
 CC platelet thrombus. The method is used to treat humans with unstable
 CC angina, stroke and/or acute myocardial infarction. The methods can be
 CC used to enact de-adhesion of osteoclasts from the bone surface to halt
 CC bone loss in a patient with osteoporosis. The methods can also be used
 CC for the de-adhesion of angiogenic endothelial cells in a patient with a
 CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
 CC retinopathy, psoriasis. The methods can also be used to treat tumours,
 CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
 CC bowel disease, or organ transplant rejection, and asthma. The methods can
 CC be used for the dissolution of pre-formed platelet aggregates, which is a
 CC departure from the current strategy of treatment prior to formation of
 CC vascular occlusions. The present sequence represents an Integrin 11gand
 CC dissociator (ILD) that can be used in the method of the invention.

SO Sequence 5 AA:

Query Match 100.0%; Score 23; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
 DB 1 eildv 5

RESULT 5

AAV80488
 ID AAV80488 standard; peptide; 5 AA.

XX
AC AAY80488;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cell adhesion peptide #23.
XX
KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
XX
OS Synthetic.
XX
PN WO200004941-A1.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16800.
XX
PR 24-JUL-1998; 98US-0122348.
XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX
PI Budny JA;
XX
DR WPI; 2000-195084/17.
XX
PT System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption -
XX
PS Claim 14; page 32; 44pp; English.
XX
CC The invention relates to a novel system for reconstitution of osseous
CC tissue comprising a scaffold carrying a compound (i) that promotes
CC bone formation and a component that decreases bone resorption (ii).
CC (i) induces migration and adhesion of osteoblasts and osteoclasts and
CC (ii) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (i) is preferably selected from: selectin or selectin binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC plasminogen activator inhibitors, protease inhibitors and
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (i) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.
XX
SQ Sequence 5 AA;
XX

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
DB 1 elldv 5

RESULT 6
AAY77442
ID AAY77442 standard; peptide; 5 AA.
XX
AC AAY77442;
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CSI-derived peptide #33.
XX

KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Mammalia.
XX
PN WO200002903-A1.
XX
PD 20-JAN-2000.
XX
PF 15-DEC-1998; 98WO-US26605.
XX
PR 10-JUL-1998; 98US-0113689.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Arrhenius TS, Ellices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX
DR WPI; 2000-182213/16.
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders -
XX
PS Disclosure; Fig 2; 243pp; English.
XX
CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAY77410).
XX
SQ Sequence 5 AA;
XX

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
DB 1 elldv 5

RESULT 7
AAY69619
ID AAY69619 standard; peptide; 5 AA.
XX
AC AAY69619;
XX
DT 19-APR-2000 (first entry)
XX
DE VLA-4 inhibitor peptide #2.
XX

KM LDV Reptide: VLA-4 inhibitor: very late antigen: alpha-4-beta-1;
KM CD49b/CD29: cell adhesion: arylalkyl azolyalkanoic acid derivative;
KM arylureidoalkyl azolyalkanoic acid derivative; inflammatory disorder;
KM autoimmune disorder; respiratory disorder; LDV motif.
XX
OS Synthetic.
XX
PN WO200000477-A1.
XX
PD 06-JAN-2000.
XX
XX 31-MAY-1999: 99MO-IB00973.
XX
XX 30-JUN-1998: 98US-0091180.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Duplantier AJ, Millic AJ, Chupak LS;
DR WPI: 2000-126762/11.
XX
PT Arylalkyl and arylureidoalkyl azolyalkanoic acid derivatives
XX
PS Disclosure: Page 2: 120pp: English.
XX
CC The invention relates to novel arylalkyl and arylureidoalkyl
CC azolyalkanoic acid derivatives and related compounds (I), and their
CC salts and prodrugs. These are are integrin inhibitors, specifically of
CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
CC inducible cell surface protein VCAM-1 (vascular cell adhesion
CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
CC and consequent or associated pathogenic processes mediated by VLA-4, and
CC may therefore be useful in the treatment and prevention of inflammatory,
CC autoimmune, or respiratory disorders. These include asthma, arthritis,
CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
CC inflammatory bowel disease. Sequences AAY69618-Y69620 represent peptides
CC derived from the VLA-4-binding domain of the FN CS-1 region which
CC contain the LDV motif and are known to inhibit fibronectin-dependent
CC cell adhesion.
XX
XX
SQ Sequence 5 AA:
OY 1 elldv 5
DB 1 elldv 5
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
RESULT 8
AAB73465 standard; peptide: 5 AA.
ID AAB73465:
XX
AC AAB73465:
XX
DT 02-JUL-2001 (first entry)
XX
DE Fibronectin VLA-4 binding domain-derived pentapeptide #1.
XX
KM Integrin antagonist: VLA-4 antagonist: alpha-4-beta-1 integrin;
KM very late antigen: antibody: kidney disease: chronic renal failure;
KM end-stage renal disease: chronic diabetic nephropathy;
KM diabetic glomerulopathy: diabetic renal hypertrophy;
KM hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
KM chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
KM nephrotic; cell adhesion inhibition; fibronectin CS-1 region.
XX
OS Unidentified.

XX
PN WO200119396-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000: 2000MO-US25140.
XX
XX 14-SEP-1999: 99US-0153826.
XX
PR 14-SEP-1999: 99US-0153826.
XX
PA (BIOJ) BIOGEN INC.
XX
PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY
XX
PI Allen A, Pusey C, Lobb R;
XX
DR WPI: 2001-273408/28.
XX
PT Treating a mammal in, or at a risk of developing, chronic renal
PT failure, involves administering at least one integrin antagonist to the
PT mammal
XX
PS Disclosure: Page 24: 62pp: English.
XX
CC The invention relates to a method for treating a mammal with,
CC or at risk of developing, chronic renal failure, involving the
CC administration of at least one integrin antagonist. The integrin
CC antagonists that may be used in the method include antagonists of
CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
CC containing integrins. In particular, the antagonists are antibodies
CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
CC The method of the invention may be used to treat chronic renal failure,
CC end-stage renal disease, chronic diabetic nephropathy, diabetic
CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
CC peptides derived from the VLA-4 binding domain (CS-1 region) of
CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
CC therefore be used in the method of the invention.
XX
XX
SQ Sequence 5 AA:
OY 1 elldv 5
DB 1 elldv 5
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
RESULT 9
AAB91966 standard; peptide: 5 AA.
ID AAB91966:
XX
AC AAB91966:
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SFO ID NO:1142.
XX
KM Protection: endogenous therapeutic peptide; peptidase: conjugation;
KM blood component: modification: succinimidyl: maleimido group: amino;
KM hydroxyl: thiol: hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2000069900-A2.
XX
PD 23-NOV-2000.

XX 17-MAY-2000; 2000MO-US13576.
 PF 17-MAY-1999; 99US-0134406.
 XX 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX (CONJ-) CONJUCHEM INC.
 PA Bridon DF, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 PI WPI; 2001-112059/12.
 DR
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 PS Disclosure; Page 569; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 CC
 SO Sequence 5 AA:
 Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 elldv 5
 Db 1 elldv 5
 RESULT 10
 AAB50876
 ID AAB50876 standard; peptide; 5 AA.
 AC AAB50876;
 XX
 DT 19-MAR-2001 (first entry)
 DE Integrin recognition peptide sequence #3.
 XX
 KW Integrin: transmembrane protein; alpha4 integrin inhibitor;
 KW paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
 KW multiple sclerosis; asthma; atherosclerosis; wound healing.
 XX
 OS unidentified.
 XX
 PN WO200073342-A1.
 PD 07-DEC-2000.
 XX
 PF 01-JUN-2000; 2000MO-US15153.
 XX
 PR 01-JUN-1999; 99US-0323447.
 XX

PA (SCRI) SCRIPPS RES INST.
 XX
 PI Ginsberg MH, Pfaff M, Liu S;
 XX WPI; 2001-070959/08.
 DR
 XX
 PT Polypeptides useful in construction of structural models for
 PT identifying therapeutic compounds, comprises series of heptad repeats
 PT that mimic a transmembrane domain and cytoplasmic domain attached to
 PT heptad repeats -
 XX
 PS Disclosure; Page 2; 37pp; English.
 XX
 CC The present sequence is given in a specification relating to a
 CC polypeptide comprising a series of heptad-repeats that mimic a
 CC transmembrane domain, and a selected cytoplasmic domain attached to the
 CC heptad repeats. At least a portion of the polypeptide is prepared
 CC recombinantly or at least 1 heptad repeat in the series has a different
 CC amino acid sequence to other heptad repeats in the series. The
 CC polypeptide is useful in the construction of structural models which are
 CC useful for evaluating structure and activity of a selected occupied and
 CC clustered transmembrane protein having the selected cytoplasmic domain
 CC and for identifying therapeutic compounds. It is also useful for
 CC identifying agents as inhibitors of alpha4 integrin biological
 CC responses by contacting the structural model with paxillin or a
 CC paxillin related molecule in the presence and absence of a test agent
 CC and determining binding of paxillin or paxillin related molecule to the
 CC structural model. A decrease in binding in the presence of the test
 CC agent indicates that the test agent is an inhibitor of alpha4 integrin
 CC biological response. Inhibitors of the binding of paxillin to alpha4 are
 CC useful in blocking immune responses in conditions such as inflammatory
 CC bowel disease, arthritis, multiple sclerosis and asthma and in
 CC inhibiting atherosclerosis and scarring during wound healing.
 CC
 SO Sequence 5 AA:
 Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 elldv 5
 Db 1 elldv 5
 RESULT 11
 AAB59135
 ID AAB59135 standard; peptide; 5 AA.
 AC AAB59135;
 XX
 DT 21-MAR-2001 (first entry)
 DE Peptide #3 recognised by integrin.
 XX
 KW Heptad repeat; transmembrane domain; cytoplasmic; integrin;
 KW inflammation; thrombosis; malignancy.
 XX
 OS Synthetic.
 XX
 PN WO200073341-A1.
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000MO-US14656.
 XX
 PR 27-MAY-1999; 99US-0320907.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Ginsberg MH, Pfaff M;
 XX

DR WPI:2001-041143/05.
 XX
 PT Polypeptides useful in construction of structural models for
 PT identifying therapeutic compounds, comprises series of heptad repeats
 PT that mimic a transmembrane domain and cytoplasmic domain attached to
 PT the repeats -
 XX
 PS Disclosure: Page 2; 36pp; English.
 XX
 CC The present invention relates to a peptide with a series of
 CC heptad-repeats that mimic a transmembrane domain and a selected
 CC cytoplasmic domain attached to the heptad repeats. The invention
 CC is useful for evaluating structure and activity of a selected
 CC occupied and clustered transmembrane protein with the selected
 CC cytoplasmic domain and for identifying therapeutic compounds. It
 CC is also useful for identifying a cytoplasmic domain binding partner.
 CC It is may be used to study protein interactions with transmembrane
 CC proteins such as integrin, which can be used to treat conditions in
 CC which over activity of integrins is involved, such as inflammation,
 CC thrombosis and malignancy.
 CC
 SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eIdv 5
 ||||
 Db 1 eIdv 5

RESULT 12
 AAR9752
 ID AAR9752 standard; peptide: 5 AA.
 AC
 XX AAR9752;
 XX
 DT 02-SEP-1996 (first entry)
 XX
 DE Cyclic peptide inhibitor of alpha-4/beta-1 integrin binding to VCAM-1.
 XX
 KW Vascular cell adhesion molecule 1; Integrin; fibronectin; invasin;
 KW binding inhibitor; atherosclerosis; allergy; rheumatoid arthritis;
 KW asthma; multiple sclerosis; type 1 diabetes; cancer; cyclic;
 KW white blood cell; metastasis.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 FT Modified-site /note= "cross-link between Glu at position 1 and
 FT Val at position 5"
 FT Modified-site 5 /note= "cross-link between Glu at position 1 and
 FT Val at position 5"
 FT
 XX W09600581-A1.
 PN
 XX 11-JAN-1996.
 PD
 XX
 PF 27-JUN-1995; 95WO-US08353.
 XX
 PR 29-JUN-1994; 94US-0268192.
 XX
 PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 XX
 PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
 XX WPI: 1996-077338/08.
 DR
 XX Isolated, purified cyclic peptide which inhibits binding of alpha-4

PT beta-1 integrin to VCAM-1 or fibronectin - useful for treating e.g.
 PT atherosclerosis or allergy
 XX
 XX
 PS Claim 6; Page 28; 51pp; English.
 XX

CC AAR9746-R99785 are cyclic peptides which selectively inhibit binding
 CC of alpha4beta1 integrin to proteins such as vascular cell adhesion
 CC molecule 1 (VCAM-1), fibronectin and invasin. Due to this action the
 CC peptides are useful in pharmaceutical preps. for the treatment of
 CC such ailments as asthma, atherosclerosis, rheumatoid arthritis,
 CC allergy, multiple sclerosis, type 1 diabetes and certain cancers
 CC (e.g. leukaemia, melanoma, lymphoma and sarcoma), as cell adhesion
 CC involving the alpha4beta1 integrin is believed to be involved in
 CC metastasis.
 CC
 SQ Sequence 5 AA;

Query Match 82.6%; Score 19; DB 17; Length 5;
 Best Local Similarity 80.0%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 eIdv 5
 ||||
 Db 1 eIdv 5

RESULT 13
 AAY77441
 ID AAY77441 standard; peptide: 4 AA.
 AC
 XX AAY77441;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fibronectin CSI-derived peptide #32.
 XX
 XX
 KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
 XX
 OS Mammalia.
 XX
 PN W0200002903-A1.
 FM
 XX 20-JAN-2000.
 PD
 XX 15-DEC-1998; 98WO-US26605.
 XX
 PF 10-JUL-1998; 98US-0113689.
 XX
 PR (CYTE-) CYTEL CORP.
 XX
 PA
 XX Arrhenius TS, Ellices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
 PI WPI: 2000-182213/16.
 DR
 XX New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders -
 XX
 XX
 PS Disclosure: Fig 2; 243pp; English.
 XX
 XX

CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and

CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAY77410).

CC Sequence 4 AA;

CC XX

CC XX

Query Match 78.3%; Score 18; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6,4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1ldv 5
1111
Db 1 1ldv 4

RESULT 14

AAY51252

ID AAY51252 standard; peptide: 4 AA.

AC AAY51252;

DT 14-APR-2000 (first entry)

XX Cyclizing peptide 1.

DE Cyclization; propanesulfonic acid anhydride; somatostatin agonist;

KW L-363,301.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 3 /note= "Asp(O-tBu)"

FT Modified-site 4 /note= "Val-NH(CH2)5COOH"

FT DE19824449-Al.

XX 02-DEC-1999.

XX 30-MAY-1998; 98DE-1024449.

XX 30-MAY-1998; 98DE-1024449.

XX (CLRN) CLARIANT GMBH.

XX Mollenkopf CC, Henklein P;

XX WPI; 2000-107180/10.

XX Cyclization of penta- or hexapeptides, e.g. to prepare somatostatin

XX agonist -

XX Claim 2; Page 4; fpp; German.

CC This invention describes a novel method for the cyclization of penta- or
CC hexapeptides which is effected by reaction with propanesulfonic acid
CC anhydride (1). The process is especially useful for cyclizing
CC H-Phe-D-Trp-Ala-Thr(tBu)-Phe-Pro-OH to obtain the somatostatin agonist
CC L-363,301, or for cyclizing H-Ile-Leu-Asp(OtBu)-Val-NH(CH2)5COOH. The
CC process gives higher yields than prior art processes. This sequence

CC represents a peptide used to illustrate the method of the invention.
XX
SQ Sequence 4 AA;

Query Match 78.3%; Score 18; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6,4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1ldv 5
1111
Db 1 1ldv 4

RESULT 15

AAW01724

ID AAW01724 standard; peptide: 5 AA.

AC AAW01724;

DT 16-APR-1997 (first entry)

XX Inhibitor of fibronectin CS-1 peptide and VLA-4 receptor binding.

XX fibronectin; high affinity; CS-1; recognition sequence; VLA-4;

KW alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor;

KW leukocyte trafficking function; peptidomimetic; treatment; asthma;

KW rheumatoid arthritis; osteoarthritis; allograft rejection;

XX skin inflammation; central nervous system demyelinating disease.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "optionally D-Ile"

FT Modified-site 5 /note= "Pro, D-Pro-NH2 or Pro-NH2"

FT W09515973-Al.

XX 15-JUN-1995.

XX 05-DEC-1994; 94WO-US13943.

XX 02-DEC-1994; 94US-0164101.

XX 06-DEC-1993; 93US-0164101.

XX (CYTE-) CYTEL CORP.

XX Arrhenius TS, Ellices MJ, Gaeta FCA;

XX WPI; 1995-224284/29.

XX New peptide mimics of fibronectin CS-1 sequence - inhibit

XX interaction of endothelial cells and VLA-4 carrying inflammatory

XX cells, for treating or preventing asthma, arthritis etc.

XX Disclosure; Page 37; 103pp; English.

CC The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an
CC active participant in leukocyte trafficking functions. Binding of
CC inflammatory cells to endothelial cells that express the CS-1 portion
CC (AAW01703) of fibronectin on their surfaces can be inhibited by CS-1
CC peptidomimetic cpds. of minimal length. A minimal essential sequence for
CC specific VLA-4 recognition of CS-1 has been identified as the tripeptide
CC LDV. A generic peptidomimetic inhibits the binding of Jurkat cells
CC (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay
CC in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to
CC or up to about 3000-fold greater than the inhibition in the binding
CC exhibited by AAW01705. CS-1 mediated inflammation, e.g. asthma,
CC rheumatoid arthritis, osteoarthritis, allograft rejection, skin
CC inflammation or central nervous system demyelinating disease, can be
CC treated by the peptidomimetics. AAW01706-27 are exemplary inhibitor

CC peptides.
XX
SQ Sequence 5 AA:

Query Match 78.3%; Score 18; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 11dv 5
 | | | | |
Db 1 11dv 4

RESULT 16
AAW45730
ID AAW45730 standard; peptide; 5 AA.
AC AAW45730:
XX
XX
DT 17-JUN-1998 (first entry)
XX
DE Precursor peptide #1.
XX
KM Cyclic peptide; dimeric peptide; vascular cell adhesion molecule-1;
KW VCAM-1; fibronectin; integrin; rheumatoid arthritis; asthma;
XX multiple sclerosis; VLA-4; very late antigen-4; precursor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 3 /note="asp(OBut)"
FT Modified-site 5 /note="Piperazinyl-1-yl-acetic acid"
FT FT
XX
XX
PN MO9702289-A1.
XX
PD 23-JAN-1997.
XX
PF 02-JUL-1996; 96WO-GB01580.
XX
PR 01-JUN-1996; 96GB-0011470.
PR 06-JUL-1995; 95GB-0013798.
XX
XX (ZENE) ZENECA LTD.
XX
PI Dutta AS:
XX
XX
DR WPI; 1997-108916/10.
XX
XX
XX Cyclic octa-peptide comprising dimeric tetra-peptides joined by two
PT peptide mimetic linking gps. - block interaction of VCAM-1 and/or
PT fibronectin with integrin VLA4, used in treating arthritis, asthma
PT and multiple sclerosis
XX
XX
XX Example 1; Page 30; 82pp; English.
XX
XX The present sequence represents a precursor peptide. The invention
CC relates to cyclic peptides which block the interaction of protein
CC ligand VCAM-1 (vascular cell adhesion molecule-1) to its integrin
CC receptor VLA-4 (very late antigen-4), thereby modulating T-cell
CC proliferation, B-cell localisation to germinal centres and adhesion of
CC activated T-cells and eosinophils to endothelial cells. These peptides
CC are thus of use in treating diseases associated with these processes,
CC including rheumatoid arthritis, multiple sclerosis and asthma, melanoma
CC cell invasion in metastasis, autoimmune diabetes, colitis, autoimmune
CC encephalomyelitis, atherosclerosis, peripheral vascular or
CC cardiovascular disease, nephritis, allograft rejection, psoriasis,
CC restenosis, myocarditis, and inflammatory bowel disease.
XX
SQ Sequence 5 AA:

Query Match 78.3%; Score 18; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 11dv 5
 | | | | |
Db 1 11dv 4

RESULT 17
AAV77428
ID AAV77428 standard; peptide; 5 AA.
XX
XX AAV77428:
XX
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CS1 peptidomimetic #19.
XX
XX Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
XX inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5 /note="C-terminal amide, D-form residue"
FT FT
XX
XX
PN WO200002903-A1.
XX
XX 20-JAN-2000.
PD
XX
XX 15-DEC-1998; 98WO-US26605.
PF
XX
PR 10-JUL-1998; 98US-0113689.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX
XX WPI; 2000-182213/16.
XX
XX
XX New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders
XX
XX
XX Disclosure; Page 136; 243pp; English.
XX
XX
XX The invention relates to peptidomimetic compounds (AAV77415-V77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAV77415-V77433
CC represent specific examples of the inhibitory peptidomimetics of the
CC invention.

XX Sequence 5 AA:
 S0

Query Match
 Best Local Similarity 78.3%; Score 18; DB 21; Length 5;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1ldv 5
 1111
 Db 1 1ldv 4

RESULT 18
 AAY77431
 ID AAY77431 standard; peptide; 5 AA.
 XX
 AC AAY77431;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fibronection CS1 peptidomimetic #22.
 XX
 KW Fibronection; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 5 Location/Qualifiers
 FT /note="C-terminal amide, D-form residue"
 XX
 PN WO200002903-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 15-DEC-1998; 98WO-US26605.
 XX
 PR 10-JUL-1998; 98US-0113689.
 XX
 PA (CYTE) CYTEL CORP.
 XX
 PI Arrhenius TS, Ellices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
 XX
 DR WPI; 2000-182213/16.
 XX
 PT New peptidomimetic compounds used as cell surface fibronection
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders
 XX
 PS Disclosure; Page 136; 243pp; English.
 XX
 CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronection (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allergic rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to

CC manufacture, and are resistant to proteolysis. Sequences AAY77415-Y77433
 CC represent specific examples of the inhibitory peptidomimetics of the
 CC invention.
 XX
 S0 Sequence 5 AA:
 XX

Query Match
 Best Local Similarity 78.3%; Score 18; DB 21; Length 5;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1ldv 5
 1111
 Db 1 1ldv 4

RESULT 19
 AAR92849
 ID AAR92849 standard; peptide; 5 AA.
 XX
 AC AAR92849;
 XX
 DT 03-OCT-1996 (first entry)
 XX
 DE Cell adhesion modulatory peptide AP21.
 XX
 KW Intercellular adhesion; stimulation; inhibition; skin graft;
 KW synthetic blood vessel; coating; endothelial cell; epidermal cell;
 KW chemotactic attractor; wound healing; organ transplantation;
 KW thrombosis; arteriosclerosis; cancer metastases.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Peptide 3..5 Location/Qualifiers
 FT /label="tripeptide
 FT /note="this tripeptide is also specifically
 FT claimed"
 XX
 PN DE4430601-A1.
 XX
 PD 29-FEB-1996.
 XX
 PF 22-AUG-1994; 94DE-4430601.
 XX
 PR 22-AUG-1994; 94DE-4430601.
 XX
 PA (BEI) BEIERSDORF AG.
 XX
 PI Doerschner A, Eichner W, Kock K, Mielke H;
 XX
 DR WPI; 1996-130242/14.
 XX
 PT peptide(s) that stimulate or inhibit cell to cell adhesion - used
 PT e.g. to coat synthetic blood vessels with endothelial cells, to
 PT prepare, or increase growth of skin grafts, to prevent thrombosis
 PT etc.
 XX
 PS Claim 9; Page 14; 18pp; German.
 XX
 CC The present peptide is a specifically claimed example of a peptide
 CC which contains the highly generic sequence AA5-AA4-AA3-AA2-AA1-(AAx)n
 CC where AA5 is Gly, Ser, Asp or Asn; AA4 is Leu or Ser, AA3 is Leu, Ile,
 CC Phe or Gly; AA2 is Asp, Leu, Asn or Ser; AA1 is Gly, Pro or Asp; AAx
 CC is any amino acid and n = 0 or 1. When two or more such peptides are
 CC attached to a carrier, the product can be used for stimulating
 CC adhesion of eukaryotic cells in vitro. Particular applications include
 CC coating synthetic blood vessels with endothelial cells, preparing skin
 CC grafts using epithelial cells or stimulating wound healing. When a
 CC single peptide is used it may inhibit intercellular adhesion, making
 CC it useful for preventing thrombosis or arteriosclerosis or to suppress
 CC cancer metastases. The peptides can also be used as chemotactic
 CC attractors and for detecting/quantifying cell-cell adhesion in vitro.

XX Sequence 5 AA:

Query Match
Best Local Similarity 73.9%; Score 17; DB 17; Length 5;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 elld 4
1:11
Db 1 elld 4

RESULT 20

AAR95707
ID AAR95707 standard; peptide; 5 AA.

AC AAR95707;

DT 03-DEC-1996 (first entry)

DE Alpha-4beta-1 integrin binding inhibitory peptide 4.

KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
inhibitor; binding; white blood cell; migration; capillary wall;
tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
CS1; CS5; HI; LDV; active site.

OS Synthetic.

PN US5510332-A.

PD 23-APR-1996.

PF 07-JUL-1994; 94US-0271830.

PR 07-JUL-1994; 94US-0271830.

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

PI Beck PJ, Kogan TP, Ren K, Vanderslice P;

DR WPI; 1996-221274/22.

PT New peptide(s) based on the LDV domain of fibronectin - used for
inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT fibronectin or invasion

PS Claim 2; Column 15; 35pp; English.

XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
XX surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognizes and binds to the integrin alpha-4beta-1 (IA4B1) or
CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white
CC blood cells flooding to the scene, causing widespread tissue damage.
CC Cpd's capable of blocking this process may be beneficial as therapeutic
CC agents. IA4B1 also recognizes the extracellular matrix glycoprotein
CC fibronectin. Three distinct IA4B1-binding sites have been identified
CC within fibronectin. One site is found in the HepII region and is
CC expressed in all isoforms; two others (CS1 and CS5) are present in the
CC alternatively spliced type III connecting segments. CS1 has the higher
CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC peptide that include the LDV domain presented in such a way by its novel
CC flanking sequence to produce a potent inhibitor of IA4B1 binding.

SO Sequence 5 AA:

Query Match
Best Local Similarity 69.6%; Score 16; DB 17; Length 5;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 elldv 5
1:111
Db 1 ewldv 5

RESULT 21

AAR95716
ID AAR95716 standard; peptide; 5 AA.

AC AAR95716;

DT 04-DEC-1996 (first entry)

DE Alpha-4beta-1 integrin binding inhibitory peptide 13.

KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
inhibitor; binding; white blood cell; migration; capillary wall;
tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
CS1; CS5; HI; LDV; active site.

OS Synthetic.

FT Key Location/Qualifiers
FT Modified-site 10
FT /note="Val-NH2"

PN US5510332-A.

PD 23-APR-1996.

PF 07-JUL-1994; 94US-0271830.

PR 07-JUL-1994; 94US-0271830.

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

PI Beck PJ, Kogan TP, Ren K, Vanderslice P;

DR WPI; 1996-221274/22.

PT New peptide(s) based on the LDV domain of fibronectin - used for
inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT fibronectin or invasion

PS Claim 4; Column 19-20; 35pp; English.

XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
XX surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognizes and binds to the integrin alpha-4beta-1 (IA4B1) or
CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white
CC blood cells flooding to the scene, causing widespread tissue damage.
CC Cpd's capable of blocking this process may be beneficial as therapeutic
CC agents. IA4B1 also recognizes the extracellular matrix glycoprotein
CC fibronectin. Three distinct IA4B1-binding sites have been identified
CC within fibronectin. One site is found in the HepII region and is
CC expressed in all isoforms; two others (CS1 and CS5) are present in the
CC alternatively spliced type III connecting segments. CS1 has the higher
CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC peptide that include the LDV domain presented in such a way by its novel
CC flanking sequence to produce a potent inhibitor of IA4B1 binding.

SO Sequence 5 AA:

Query Match 69.6%; Score 16; DB 17; Length 5;
 Best Local Similarity 80.0%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 eildv 5
 | | | |
 Db 1 ewldv 5

RESULT 22

AAR95717
 ID AAR95717 standard; peptide; 5 AA.

AC AAR95717;

DT 04-DEC-1996 (first entry)

DE Alpha-4Beta-1 integrin binding inhibitory peptide 14.

XX VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
 KW inhibitor; binding; white blood cell; migration; capillary wall;
 KM tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
 KW CSI; CS5; HI; LDV; active site.

XX Synthetic.

XX US5510332-A.

PD 23-APR-1996.

XX 07-JUL-1994; 94US-0271830.

XX 07-JUL-1994; 94US-0271830.

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

PI Beck PJ, Kogan TP, Ren K, Vanderslice P;

DR WPI; 1996-221274/22.

XX New peptide(s) based on the LDV domain of fibronectin - used for
 PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
 PT fibronectin or invasin

PS Claim 4; Column 21-22; 35pp; English.

XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
 CC surface of endothelial cells that line the interior wall of capillaries.
 CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
 CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
 CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
 CC white blood cells to adhere to the capillary wall in areas where the
 CC tissue surrounding the capillary has been infected or damaged. Sometimes
 CC this white blood cell migration can become uncontrolled, with white
 CC blood cells flooding to the scene, causing widespread tissue damage.
 CC Cpd's capable of blocking this process may be beneficial as therapeutic
 CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
 CC fibronectin. Three distinct IA4B1-binding sites have been identified
 CC within fibronectin. One site is found in the HepII region and is
 CC expressed in all isoforms; two others (CS1 and CS5) are present in the
 CC alternatively spliced type III connecting segments. CS1 has the higher
 CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
 CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
 CC peptide that include the LDV domain presented in such a way by its novel
 CC flanking sequence to produce a potent inhibitor of IA4B1 binding.

XX Sequence 5 AA:

Query Match 69.6%; Score 16; DB 17; Length 5;
 Best Local Similarity 80.0%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 eildv 5
 | | | |
 Db 1 ewldv 5

RESULT 23

AAR9748
 ID AAR9748 standard; peptide; 5 AA.

AC AAR9748;

DT 02-SEP-1996 (first entry)

DE Cyclic peptide inhibitor of alpha-4/beta-1 integrin binding to VCAM-1.

XX Vascular cell adhesion molecule 1; integrin; fibronectin; invasin;
 KW binding inhibitor; atherosclerosis; allergy; rheumatoid arthritis;
 KW asthma; multiple sclerosis; type 1 diabetes; cancer; cyclic;
 KW white blood cell; metastasis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note- "cross-link between Glu at position 1 and
 FT Val at position 5"

FT Modified-site 5 /note- "cross-link between Glu at position 1 and
 FT Val at position 5"

XX W09600581-A1.

XX 11-JAN-1996.

XX 27-JUN-1995; 95WO-US08353.

XX 29-JUN-1994; 94US-0268192.

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

PI Beck PJ, Kogan TP, Ren K, Vanderslice P;

DR WPI; 1996-077338/08.

XX Isolated, purified cyclic peptide which inhibits binding of alpha-4
 PT beta-1 integrin to VCAM-1 or fibronectin - useful for treating e.g.
 PT atherosclerosis or allergy

PS Claim 6; Page 27; 51pp; English.

XX AAR9746-R99785 are cyclic peptides which selectively inhibit binding
 CC of alphabeta1 integrin to proteins such as vascular cell adhesion
 CC molecule 1 (VCAM-1), fibronectin and invasin. Due to this action the
 CC peptides are useful in pharmaceutical preps. for the treatment of
 CC such ailments as asthma, atherosclerosis, rheumatoid arthritis,
 CC allergy, multiple sclerosis, type 1 diabetes and certain cancers
 CC (e.g. leukaemia, melanoma, lymphoma and sarcoma), as cell adhesion
 CC involving the alphabeta1 integrin is believed to be involved in
 CC metastasis.

XX Sequence 5 AA:

Query Match 69.6%; Score 16; DB 17; Length 5;
 Best Local Similarity 80.0%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 eildv 5
 | | | |
 Db 1 ewldv 5

RESULT 24

```

AAW45731
ID AAW45731 standard; peptide; 5 AA.
XX
AC AAW45731;
XX
XX
DT 17-JUN-1998 (first entry)
XX
DE Precursor peptide #2.
XX
KW Cyclic peptide; dimeric peptide; vascular cell adhesion molecule-1;
KM VCAM-1; fibronectin; integrin; rheumatoid arthritis; asthma;
KM multiple sclerosis; VLA-4; very late antigen-4; precursor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 1
FT Modified-site 3/note="D-form residue"
FT Modified-site 5/note="Asp(Obut)"
FT Modified-site 5/note="Piperazinyl-1-yl-acetic acid"
XX
XX MO9702289-A1.
XX
XX 23-JAN-1997.
XX
XX 02-JUL-1996; 96MO-GH01580.
XX
XX 01-JUN-1996; 96GB-0011470.
XX 06-JUL-1995; 95GB-0013798.
XX
XX (ZENEC) ZENECA LTD.
XX
XX Dutta AS;
XX
XX WPI; 1997-108916/10.
XX
XX Cyclic octa-peptide comprising dimeric tetra-peptides joined by two
XX peptide mimetic linking gps. - block interaction of VCAM-1 and/or
XX fibronectin with integrin VLA4, used in treating arthritis, asthma
XX and multiple sclerosis
XX
XX Example 1; Page 30; 82pp; English.
XX
XX The present sequence represents a precursor peptide. The invention
XX relates to cyclic peptides which block the interaction of protein
XX ligand VCAM-1 (vascular cell adhesion molecule-1) to its integrin
XX receptor VLA-4 (very late antigen-4), thereby modulating T-cell
XX proliferation, B-cell localisation to germinal centres and adhesion of
XX activated T-cells and eosinophils to endothelial cells. These peptides
XX are thus of use in treating diseases associated with these processes,
XX including rheumatoid arthritis, multiple sclerosis and asthma, melanoma
XX cell invasion in metastasis, autoimmune diabetes, colitis, autoimmune
XX encephalomyelitis, atherosclerosis, peripheral vascular or
XX cardiovascular disease, nephritis, allograft rejection, psoriasis,
XX restenosis, myocarditis, and inflammatory bowel disease.
XX
XX Sequence 5 AA:
SQ

```

```

Query Match 69.6%; Score 16; DB 18; Length 5;
Best Local Similarity 75.0%; Pred. NO. 6.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 2 11dV 5
DB 1 11dV 4

```

```

RESULT 25
AAV30308
ID AAV30308 standard; peptide; 5 AA.

```

```

XX
AC AAV30308;
XX
XX 23-NOV-1999 (first entry)
XX
XX Angiopoietin derived peptide #23.
XX
DE Angiopoietin derived peptide #23.
XX
KW Angiogenesis; tumour; metastasis; wound healing; diabetic retinopathy;
KM rheumatoid arthritis; psoriasis; cancer; blood supply; imaging;
KM treatment; angiopoietin; Tie-1; Tie-2; TPCK Trypsin; protease;
KM receptor tyrosine kinase.
XX
OS Synthetic.
XX
XX MO9940947-A2.
XX
XX 19-AUG-1999.
XX
XX 11-FEB-1999; 99MO-CA00101.
XX 11-FEB-1998; 98US-0074420.
XX
XX (RESO-) RESOLUTION PHARM INC.
XX
XX Eshima D, Fauconnier T, Pollak A, Thornback J;
XX WPI; 1999-527342/44.
XX
XX Angiogenesis targeting molecules, for, e.g. detecting and treating
XX cancer
XX
XX Example 16; Page 50; 70pp; English.
XX
XX Sequences AAV30286-Y30310 and AAV34151-Y34156 are peptides derived from
XX the angiotensin through cleavage by the proteases TPCK Trypsin or
XX Staphylococcus aureus protease. The angiotensins bind to the receptor
XX tyrosine kinase Tie-2 which is upregulated during angiogenesis.
XX Angiopoietin 1 (Ang 1) is ubiquitously expressed and interacts with
XX Tie-2 on endothelial cells and early haemopoietic cells. Angiopoietin 2
XX (Ang 2) is homologous to Ang 1 and competitively inhibits Ang 1
XX interaction with Tie-2. Angiogenesis is the process involved in creating
XX a blood supply to a tumour. The peptides are used in a compound that
XX binds to sites of angiogenesis. The compound consists of a chelator
XX moiety capable of complexing a radionuclide metal or a moiety capable of
XX binding to a halogen group, and an angiogenesis targeting molecule. The
XX peptides are incorporated in the angiogenesis targeting molecule. The
XX compounds are used for imaging and treating angiogenesis, and also to
XX detect, stage and treat tumours and metastases. Angiogenesis is also
XX required for wound healing and conditions such as diabetic retinopathy,
XX rheumatoid arthritis and psoriasis, therefore the compounds may also be
XX useful in the treatment of these conditions.
XX
XX Sequence 5 AA:
SQ

```

```

Query Match 69.6%; Score 16; DB 20; Length 5;
Best Local Similarity 75.0%; Pred. NO. 6.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 11dV 4
DB 2 11dV 5

```

```

RESULT 26
AAR82907
ID AAR82907 standard; peptide; 3 AA.
XX
AC AAR82907;
XX
XX 20-DEC-1995 (first entry)
XX
DE Non-RGD, non-TISGR cancer metastasis inhibitory peptide #1.

```

XX	Cancer metastasis: adhesive peptide; core sequence; dextran; cancer;
KW	water soluble polysaccharide; metastasis; wound; immunogenicity.
XX	
OS	Synthetic.
XX	
PN	JP07089999-A.
XX	
PD	04-APR-1995.
XX	
PF	17-SEP-1993; 93JP-0254779.
XX	
PR	17-SEP-1993; 93JP-0254779.
XX	
PA	(JABG) NIPPON ZEON KK.
XX	
DR	WPI, 1995-167254/22.
XX	
PT	Cancer metastasis inhibitive peptide derivs. - useful for inhibition
PT	of cancer metastasis, healing of wounds and regulation of
PT	immunogenicity.
XX	
PS	Disclosure; Page 3; 6pp; Japanese.
XX	
CC	The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
CC	inhibit cancer metastasis. They are composed of an adhesive peptide
CC	with a core sequence selected from: RGD (AAR70472-85), YIGSR
CC	(AAR70486-90) or other sequence (AAR82907-24), linked to a water soluble
CC	polysaccharide, preferably a water soluble dextran, at the C-terminus.
CC	The peptides are useful in inhibiting cancer metastasis, healing wounds
CC	and the regulation of immunogenicity.
XX	
SQ	Sequence 3 AA;
XX	
Query Match	60.9%; Score 14; DB 16; Length 3;
Best Local Similarity	100.0%; Pred. No. 6,4e+05;
Matches 3; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	3 Ldv 5
Db	1 Ldv 3
XX	
RESULT 27	
AAW25187	
ID	AAW25187 standard; peptide; 3 AA.
XX	
AC	AAW25187;
XX	
DT	05-JAN-1998 (first entry)
XX	
DE	LDV-peptide capable of binding cell adhesion molecules.
XX	
KW	LDV; leucine; aspartic acid; valine; cell adhesion molecule;
KW	binding; bladder irrigation; tumour removal; endoscopic operation;
KW	transurethral resection; cancer; neoplasia.
XX	
OS	Synthetic.
XX	
PN	DE19529909-A1.
XX	
PD	20-FEB-1997.
XX	
PF	15-AUG-1995; 95DE-1029909.
XX	
PR	15-AUG-1995; 95DE-1029909.
XX	
PA	(FRPP) FRIESENHUS AG.
XX	
PI	Boehle A;
XX	
DR	WPI; 1997-133793/13.

XX	Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
PT	adhesion molecules
XX	
XX	Claim 6; Page 8; 8pp; German.
CC	AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
CC	The peptides are capable of binding to cell adhesion molecules and
CC	are used in aqueous irrigation solutions for use during and after
CC	endoscopic operations. Preferred irrigation solutions are
CC	electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
CC	oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
CC	GPRA, VTL, YIGSR, KQAGDV and/or RBDV (given in one letter amino acid
CC	code). The solutions are especially used for irrigating the bladder
CC	during and after tumour removal by transurethral resection. The
XX	peptides protect against recurrence of tumours.
SQ	Sequence 3 AA;
QY	Query Match 60.9%; Score 14; DB 18; Length 3;
	Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 Idv 3
XX	
RESULT 28	
ID	AAAB01568 standard; peptide; 3 AA.
XX	
AC	AAAB01568;
XX	
XX	08-NOV-2000 (first entry)
XX	
DE	Cell binding domain of Fibronectin.
XX	
KW	Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
KW	sealant; tissue engineering; wound healing; scaffold;
KW	cell transplant; adhesion prevention; cell migration; collagenase;
KW	plasma; elastase.
XX	
OS	Synthetic.
XX	
PN	WO200044808-A1.
XX	
PD	03-AUG-2000.
XX	
PF	01-FEB-2000; 2000WO-US02608.
XX	
PR	01-FEB-1999; 99US-0118093.
XX	
PA	(HUBB/) HUBBELL J A.
XX	
PI	Hubbell Jb, Elbert D, Lutolf M, Pratt A, Schoenmakers R;
PI	Tirelli M, Vernon B;
XX	
DR	WPI; 2000-524289/47.
PT	Producing polymeric biomaterials by polymerizing two or more precursor
PT	components (e.g. polymer, protein or peptide) of the biomaterial,
PT	useful for delivering therapeutic molecules to a subject and as
PT	adhesives or sealants
XX	
PS	Disclosure; Page 52; 119pp; English.
XX	
CC	A method of making polymeric biomaterials is described comprising
CC	combining two or more precursor components (e.g. polymer, protein or
CC	peptide) of the biomaterial under conditions that allow
CC	polymerisation of the two components. Polymerisation occurs through
CC	self selective reaction between a strong nucleophile and a conjugated


```

XX AC AAR95728;
XX DT 04-DEC-1996 (first entry)
XX DE Alpha-4beta-1 integrin binding inhibitory peptide 25.
XX KM VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
XX KM inhibitor; binding; white blood cell; migration; capillary wall;
XX KM tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
XX KM CSI; CS5; HL; LDV; active site.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /note="Val-NH2"
XX FT
XX PN US5510332-A.
XX PD 23-APR-1996.
XX PF 07-JUL-1994; 94US-0271830.
XX PR 07-JUL-1994; 94US-0271830.
XX PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
XX DR WPI; 1996-221274/22.
XX PT New peptide(s) based on the LDV domain of fibronectin - used for
XX PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
XX PT fibronectin or invasion
XX PS Claim 4; Column 27-28; 35pp; English.
XX CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
XX CC surface of endothelial cells that line the interior wall of capillaries.
XX CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
XX CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
XX CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
XX CC white blood cells to adhere to the capillary wall in areas where the
XX CC tissue surrounding the capillary has been infected or damaged. Sometimes
XX CC this white blood cell migration can become uncontrolled, with white
XX CC blood cells flooding to the scene, causing widespread tissue damage.
XX CC Ccbs. capable of blocking this process may be beneficial as therapeutic
XX CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
XX CC fibronectin. Three distinct IA4B1-binding sites have been identified
XX CC within fibronectin. One site is found in the HepII region and is
XX CC expressed in all isoforms; two others (CS1 and CS5) are present in the
XX CC alternatively spliced type III connecting segments. CS1 has the higher
XX CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
XX CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
XX CC peptide that include the LDV domain presented in such a way by its novel
XX CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX SQ Sequence 4 AA:

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Query Match 60.9%; Score 14; DB 17; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3 Idv 5
   111
Db 2 Idv 4

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RESULT 34
 AAR95731
 ID AAR95731 standard; peptide; 4 AA.

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XX AC AAR95731;
XX DT 04-DEC-1996 (first entry)
XX DE Alpha-4beta-1 integrin binding inhibitory peptide 28.
XX KM VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
XX KM inhibitor; binding; white blood cell; migration; capillary wall;
XX KM tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
XX KM CSI; CS5; HL; LDV; active site.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /note="Val-NH2"
XX FT
XX PN US5510332-A.
XX PD 23-APR-1996.
XX PF 07-JUL-1994; 94US-0271830.
XX PR 07-JUL-1994; 94US-0271830.
XX PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
XX DR WPI; 1996-221274/22.
XX PT New peptide(s) based on the LDV domain of fibronectin - used for
XX PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
XX PT fibronectin or invasion
XX PS Claim 4; Column 27-28; 35pp; English.
XX CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
XX CC surface of endothelial cells that line the interior wall of capillaries.
XX CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
XX CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
XX CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
XX CC white blood cells to adhere to the capillary wall in areas where the
XX CC tissue surrounding the capillary has been infected or damaged. Sometimes
XX CC this white blood cell migration can become uncontrolled, with white
XX CC blood cells flooding to the scene, causing widespread tissue damage.
XX CC Ccbs. capable of blocking this process may be beneficial as therapeutic
XX CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
XX CC fibronectin. Three distinct IA4B1-binding sites have been identified
XX CC within fibronectin. One site is found in the HepII region and is
XX CC expressed in all isoforms; two others (CS1 and CS5) are present in the
XX CC alternatively spliced type III connecting segments. CS1 has the higher
XX CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
XX CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
XX CC peptide that include the LDV domain presented in such a way by its novel
XX CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX SQ Sequence 4 AA:

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Query Match 60.9%; Score 14; DB 17; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3 Idv 5
   111
Db 2 Idv 4

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RESULT 35
 AAR95726
 ID AAR95726 standard; peptide; 4 AA.

Search completed: June 10, 2002, 06:40:39
 Job time: 241 sec

XX AAR95726;
 AC
 XX
 DT 04-DEC-1996 (first entry)
 XX
 DE Alpha-4beta-1 integrin binding inhibitory peptide 23.
 XX
 KW VCAM-1; Vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
 KM inhibitor; binding; white blood cell; migration; capillary wall;
 KM tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
 KM CSI; CS5; HI; LDV; active site.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Ac-Phe"
 FT Modified-site 4 /note= "Val-NH2"
 FT
 XX
 XX US5510332-A.
 PN
 XX
 PD 23-APR-1996.
 XX
 PF 07-JUL-1994; 94US-0271830.
 XX
 PR 07-JUL-1994; 94US-0271830.
 XX
 PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 XX
 PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
 XX
 DR WPI; 1996-221274/22.
 XX
 PT New peptide(s) based on the LDV domain of fibronectin - used for
 PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
 PT fibronectin or invasin
 PT
 XX
 PS Claim 4; Column 25-26; 35pp; English.
 XX
 CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
 CC surface of endothelial cells that line the interior wall of capillaries.
 CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
 CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
 CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
 CC white blood cells to adhere to the capillary wall in areas where the
 CC tissue surrounding the capillary has been infected or damaged. Sometimes
 CC this white blood cell migration can become uncontrolled, with white
 CC blood cells flooding to the scene, causing widespread tissue damage.
 CC CPDs. Capable of blocking this process may be beneficial as therapeutic
 CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
 CC fibronectin. Three distinct IA4B1-binding sites have been identified
 CC within fibronectin. One site is found in the Hep1 region and is
 CC expressed in all isoforms; two others (CS1 and CS5) are present in the
 CC alternatively spliced type III connecting segments. CS1 has the higher
 CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
 CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
 CC peptide that include the LDV domain presented in such a way by its novel
 CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
 CC
 XX
 SQ Sequence 4 AA;

Query Match 60.9%; Score 14; DB 17; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ldv 5
 Db 2 ldv 4

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OM protein - protein search, using sw model

Run on: June 10, 2002, 06:36:37 ; Search time 15.68 seconds
(without alignments)
7.789 Million cell updates/sec

Title: 09-251073

Perfect score: 23

Sequence: 1 e1ldv 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 17877

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	5	1 US-08-109-106-3	Sequence 3, Appli
2	23	100.0	5	1 US-08-303-162A-3	Sequence 3, Appli
3	23	100.0	5	1 US-08-634-060-3	Sequence 3, Appli
4	23	100.0	5	1 US-08-338-282-10	Sequence 10, Appli
5	23	100.0	5	1 US-08-709-515-3	Sequence 3, Appli
6	23	100.0	5	2 US-08-700-846-2	Sequence 2, Appli
7	23	100.0	5	4 US-09-146-503-3	Sequence 3, Appli
8	23	100.0	5	4 US-08-983-391-2	Sequence 2, Appli
9	23	100.0	5	4 US-08-498-237-2	Sequence 2, Appli
10	23	100.0	5	4 US-08-376-372-2	Sequence 2, Appli
11	23	100.0	5	1 PCT-US95-07542-3	Sequence 3, Appli
12	19	82.6	5	1 US-08-271-830-16	Sequence 16, Appli
13	19	82.6	5	3 US-08-860-248C-39	Sequence 39, Appli
14	19	82.6	5	3 US-09-059-111-8	Sequence 8, Appli
15	19	82.6	5	5 PCT-US95-08353-8	Sequence 8, Appli
16	18	78.3	5	1 US-08-435-286-13	Sequence 13, Appli
17	18	78.3	5	1 US-08-860-248C-14	Sequence 14, Appli
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23	18	78.3	5	3 US-08-860-248C-12	Sequence 12, Appli
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86	14	60.9	4	1 US-08-271-830-1	Sequence 1, Appli
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96	14	60.9	5	2 US-08-634-641-74	Sequence 74, Appli
97	14	60.9	5	3 US-08-860-248C-7	Sequence 7, Appli
98	14	60.9	5	3 US-08-860-248C-8	Sequence 8, Appli
99	14	60.9	5	3 US-08-860-248C-9	Sequence 9, Appli
100	14	60.9			

ALIGNMENTS

RESULT 1
US-08-109-106-3
Sequence 3, Application US/08109106
Patent No. 5475100
GENERAL INFORMATION:
APPLICANT: Kimikazu HASHINO et al.
TITLE OF INVENTION: Artificial Antibody
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/109,106
CLASSIFICATION: 536
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/725,668
FILING DATE: July 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:

AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-109-106-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 e1ldv 5
Db 1 E1LDV 5

RESULT 2
US-08-303-162A-3
Sequence 3, Application US/08303162A
Patent No. 5559099
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovesdi, Imre
APPLICANT: Brough, Douglas E.
APPLICANT: Mcvey, Duncan L.
APPLICANT: Brudner, Joseph T.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,162A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 61306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-162A-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5
DB 1 EILDV 5

RESULT 3

US-08-634-060-3
Sequence 3, Application US/08634060
Patent No. 5712136
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovacsdi, Imre
APPLICANT: Roelivink, Petrus W.
TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMAND BY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Killyk, John J.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-634-060-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5
DB 1 EILDV 5

RESULT 4

US-08-338-282-10
Sequence 10, Application US/08338282
Patent No. 5730978
GENERAL INFORMATION:
APPLICANT: Wayner, E.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage

COMPUTER: IBM PC/386 Compatible

OPERATING SYSTEM: MS-DOS 4.01

SOFTWARE: Word for Windows-t

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,282

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/814,873

FILING DATE: December 24, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/402,389

FILING DATE: September 1, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Sundsmo, John, S.

REGISTRATION NUMBER: 34,446

REFERENCE/DOCKET NUMBER: CYTE-1-6162

TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)

TELEFAX: 1-206-224-0779

TELE: 4938023

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

DESCRIPTION: EILDV

US-08-338-282-10

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5
DB 1 EILDV 5

RESULT 5

US-08-709-515-3
Sequence 3, Application US/08709515
Patent No. 5731190
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovacsdi, Imre
APPLICANT: Brough, Douglas E.
APPLICANT: Mcvey, Duncan L.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,515

FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: KILYK, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 73845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-515-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
|||||
DB 1 EILDV 5

RESULT 6
US-08-700-846-2
Sequence 2, Application US/08700846
Patent No. 5962311
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: ROELVINK, PETROS W.
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
STATE: IL
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: 21-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 74294
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-700-846-2

Query Match 100.0%; Score 23; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
|||||
DB 1 EILDV 5

RESULT 7
US-09-146-503-3
Sequence 3, Application US/09146503
Patent No. 6184206
GENERAL INFORMATION:
APPLICANT: Jeffrey W. Smith
APPLICANT: Dana D. Hu
TITLE OF INVENTION: Integrin Ligand Dissociators
FILE REFERENCE: 02046,0002
CURRENT APPLICATION NUMBER: US/09/146,503
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,463
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 3
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-146-503-3

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 elldv 5
|||||
DB 1 EILDV 5

RESULT 8
US-08-983-391-2
Sequence 2, Application US/08983391
Patent No. 6239108
GENERAL INFORMATION:
APPLICANT: Lin, Ko-Chung
APPLICANT: Adams, Steven P.
APPLICANT: Castro, Alfredo C.
APPLICANT: Zimmerman, Craig N.
APPLICANT: Cuervo, Julio Herman
APPLICANT: Lee, Wen-Cherng
APPLICANT: Hammond, Charles E.
APPLICANT: Carter, Mary Beth
APPLICANT: Almquist, Ronald G.
APPLICANT: Ensinger, Carol Lee
TITLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274/024002
CURRENT APPLICATION NUMBER: US/08/983,391
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: US 08/498,237
PRIOR FILING DATE: 1995-07-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetically generated protein
US-08-983-391-2

Query Match 100.0%: Score 23; DB 4; Length 5;
Best Local Similarity 100.0%: Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Gy 1 elldv 5
11111
Db 1 EILDV 5

RESULT 9
US-08-498-237-2
Sequence 2, Application US/08498237
Patent No. 6248713
GENERAL INFORMATION:
APPLICANT: Lin, Ko-Chung
APPLICANT: Adams, Steven P
APPLICANT: Castro, Alfredo C
APPLICANT: Zimmerman, Craig N
APPLICANT: Cuervo, Julio H
APPLICANT: Lee, Wen-Cherng
APPLICANT: Hammond, Charles E
APPLICANT: Carter, Mary B
APPLICANT: Almqvist, Ronald G
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,237
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-498-237-2

Query Match 100.0%: Score 23; DB 4; Length 5;
Best Local Similarity 100.0%: Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Gy 1 elldv 5
11111
Db 1 EILDV 5

RESULT 10
US-08-376-372-2
Sequence 2, Application US/08376372
Patent No. 6306840

GENERAL INFORMATION:
APPLICANT: Adams, Steven P
APPLICANT: Lin, Ko-Chung
APPLICANT: Lee, Wen-Cherng
APPLICANT: Castro, Alfredo C
APPLICANT: Zimmerman, Craig N
APPLICANT: Hammond, Charles E
APPLICANT: Liao, Yu-Sheng
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-376-372-2

Query Match 100.0%: Score 23; DB 4; Length 5;
Best Local Similarity 100.0%: Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Gy 1 elldv 5
11111
Db 1 EILDV 5

RESULT 11
PCT-US95-07542-3
Sequence 3, Application PC/TUS9507542
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
DOMAINS OF TRANSMEMBRANE RECEPTORS
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07542

FILING DATE: 13-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/260,514
FILING DATE: 15-JUN-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Ligand sequence recognized by integrin
PCT-US95-07542-3

Query Match 100.0%; Score 23; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
DB 1 EILDV 5

RESULT 12
US-08-271-830-16
Sequence 16, Application US/08271830
Patent No. 5510332
GENERAL INFORMATION:
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Beck, Pamela J.
TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
TITLE OF INVENTION: INTEGRIN 'A 1 TO VCAM OR FIBRONECTIN AND
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnanow, Ltd.
STREET: 180 No. 5510332th Stetson, Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,830
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5510332thrup, Thomas E.
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label="Xaa"
OTHER INFORMATION: /note="Xaa-Val-NH2."
US-08-271-830-16

Query Match 82.6%; Score 19; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 eild 4
|||||
DB 1 EILD 4

RESULT 13
US-08-860-248C-39
Sequence 39, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="D CONFIGURATION"
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="D CONFIGURATION"
US-08-860-248C-39

Query Match 82.6%; Score 19; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 eildv 5
|||||
DB 1 EILDV 5

RESULT 14
US-09-059-111-8
Sequence 8, Application US/09059111
Patent No. 6087330
GENERAL INFORMATION:
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Beck, Pamela J.
TITLE OF INVENTION: A Process To Inhibit Binding Of The
TITLE OF INVENTION: Integrin '4 ,To VCAM-1 or Fibronectin And Cyclic Peptides
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow, & Katz
STREET: 180 No. 6087330th Stetson, 2 Prudential Plaza, Suite
STREET: 4700
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,111
FILING DATE: 13-APR-1998
CLASSIFICATION: 50
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: TEX4542013205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165400
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..5
OTHER INFORMATION: /note= crosslink between Glu at
OTHER INFORMATION: position 1 and Val at position 5.
US-09-059-111-8

Query Match 82.6%; Score 19; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 eldv 5
1 111
DB 1 EFLDV 5

RESULT 15
PCT-US95-08353-8
Sequence 8, Application PC/TUS9508353
GENERAL INFORMATION:
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Beck, Pamela J.
TITLE OF INVENTION: A PROCESS TO INHIBIT BINDING OF
TITLE OF INVENTION: THE INTEGRIN '4 1 TO VCAM-1 OR
TITLE OF INVENTION: FIBRONECTIN AND CYCLIC PEPTIDES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow,
ADDRESSEE: Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08353
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas E.
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..5
OTHER INFORMATION:
OTHER INFORMATION: /note= crosslink between Glu at position 1 and
OTHER INFORMATION: Val at position 5.
PCT-US95-08353-8

Query Match 82.6%; Score 19; DB 5; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 eldv 5
1 111
DB 1 EFLDV 5

RESULT 16
US-08-435-286-13
Sequence 13, Application US/08435286
GENERAL INFORMATION:
Patent No. 5688913
GENERAL INFORMATION:
APPLICANT: Arhenius, Thomas S.
APPLICANT: Ellices, Mariano J.
APPLICANT: Gaeta, Federico C.A.
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5688913th Stetson, Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa = Pro-NH2."
US-08-435-286-13

Query Match 78.3%; Score 18; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 11dv 5
Db 1 11dv 4

RESULT 17
US-08-435-286-14
Sequence 14 Application US/08435286
Patent No. 5688913
GENERAL INFORMATION:
APPLICANT: Arthenius, Thomas S.
APPLICANT: Ellices, Mariano J.
APPLICANT: Gaeta, Federico C.A.
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5688913th Stetson, Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-435-286-14

Query Match 78.3%; Score 18; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 11dv 5
Db 1 11dv 4

RESULT 18
US-08-860-248C-1
Sequence 1, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="4-AMINO-BUTYRIC ACID"
US-08-860-248C-1

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 11dv 5
Db 1 11dv 4

RESULT 19
US-08-860-248C-2

Sequence 2, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 5
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="4-AMINO-PENTANOIC ACID"
US-08-860-248C-2

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 1ldv 5
||||
DB 1 1ldv 4

RESULT 20
US-08-860-248C-3
Sequence 3, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 5
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="6-AMINO-HEXANOIC ACID"
US-08-860-248C-3

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 1ldv 5
||||
DB 1 1ldv 4

RESULT 21
US-08-860-248C-4
Sequence 4, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 5
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="7-AMINO-HEPTANOIC ACID"
US-08-860-248C-4

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 Ildv 5
1111
Db 1 Ildv 4

RESULT 22
US-08-860-248C-5
; Sequence 5, Application US/08860248C
; Patent No. 6034056
; GENERAL INFORMATION:
; APPLICANT: DUTTA, Anand
; TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,248C
; FILING DATE: 24-JUNE-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426254.0
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505905.1
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9513904.4
; FILING DATE: 07-JUL-1995
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 5
; OTHER INFORMATION: /product="OTHER"
; OTHER INFORMATION: /note="7-AMINO-HEPTANOIC ACID"
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /product="OTHER"
; OTHER INFORMATION: /note="D CONFIGURATION"

US-08-860-248C-5

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 Ildv 5
1111
Db 1 Ildv 4

RESULT 23
US-08-860-248C-11
; Sequence 11, Application US/08860248C
; Patent No. 6034056
; GENERAL INFORMATION:
; APPLICANT: DUTTA, Anand
; TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,248C
; FILING DATE: 24-JUNE-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426254.0
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505905.1
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9513904.4
; FILING DATE: 07-JUL-1995
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /product="OTHER"
; OTHER INFORMATION: /note="N-ACETYL-D-LYSINE"
US-08-860-248C-11

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 Ildv 5
1111
Db 2 Ildv 5

RESULT 24
US-08-860-248C-12
; Sequence 12, Application US/08860248C
; Patent No. 6034056

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: GENERAL INFORMATION:
: APPLICANT: DUTTA, Anand
: TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
: NUMBER OF SEQUENCES: 122
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS WORD
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/860,248C
: FILING DATE: 24-JUNE-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9426254.0
: FILING DATE: 24-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9505905.1
: FILING DATE: 23-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9513904.4
: FILING DATE: 07-JUL-1995
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1
: OTHER INFORMATION: /product= "OTHER"
: OTHER INFORMATION: /note= "N-ACETYL-D-ORNITHINE"
US-08-860-248C-12

Query Match      78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1ldv 5
   1111
Db 2 1ldv 5

RESULT 25
US-08-860-248C-13
: Sequence 13, Application US/08860248C
: Patent No. 6034056
: GENERAL INFORMATION:
: APPLICANT: DUTTA, Anand
: TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
: NUMBER OF SEQUENCES: 122
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS WORD
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/860,248C
: FILING DATE: 24-JUNE-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9426254.0
: FILING DATE: 24-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9505905.1
: FILING DATE: 23-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9513904.4
: FILING DATE: 07-JUL-1995
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1
: OTHER INFORMATION: /product= "OTHER"
: OTHER INFORMATION: /note= "N-ACETYL-ORNITHINE"
US-08-860-248C-13

Query Match      78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 1ldv 5
   1111
Db 2 1ldv 5

RESULT 26
US-08-860-248C-14
: Sequence 14, Application US/08860248C
: Patent No. 6034056
: GENERAL INFORMATION:
: APPLICANT: DUTTA, Anand
: TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
: NUMBER OF SEQUENCES: 122
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS WORD
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/860,248C
: FILING DATE: 24-JUNE-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9426254.0
: FILING DATE: 24-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9505905.1
: FILING DATE: 23-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9513904.4
: FILING DATE: 07-JUL-1995
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "N-ACETYL-D-LYSINE"
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "D CONFIGURATION"
US-08-860-248C-14

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1ldv 5
1111
Db 2 1ldv 5

RESULT 27
US-08-860-248C-15
Sequence 15, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 5
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "4-AMINOMETHYL-BENZOIC ACID"
US-08-860-248C-15

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1ldv 5
1111
Db 1 1ldv 4

RESULT 28
US-08-860-248C-16
Sequence 16, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 5
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "(4-(2-AMINOETHYL)-IMIDAZOL-1-YL)-
ACETIC ACID"
US-08-860-248C-16

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1ldv 5
1111
Db 1 1ldv 4

RESULT 29
US-08-860-248C-20
Sequence 20, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:

APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="N-ACETYL-D-LYSINE"
US-08-860-248C-20

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 1ldv 5
DB 2 1ldv 5

RESULT 30
US-08-860-248C-21
Sequence 21, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="N-ACETYL-ORNITHINE"
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="D-CONFIGURATION"
US-08-860-248C-21

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 1ldv 5
DB 2 1ldv 5

RESULT 31
US-08-860-248C-22
Sequence 22, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4

FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="N-ACETYL-D-ORNITHINE"
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="D-CONFIGURATION"
US-08-860-248C-22

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 1ldv 5
1111
Db 2 1ldv 5

RESULT 32
US-08-860-248C-23
Sequence 23, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1

OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="N-ACETYL-LYSINE"
FEATURE:
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LOCATION: 2
OTHER INFORMATION: /product="OTHER"
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US-08-860-248C-23

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 1ldv 5
1111
Db 2 1ldv 5

RESULT 33
US-08-860-248C-24
Sequence 24, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="N-ACETYL-2,4-DIAMINO-BUTYRIC ACID"
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="D-CONFIGURATION"
US-08-860-248C-24

Query Match 78.3%; Score 18; DB 3; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 11dv 5
1111
DB 2 1LDV 5

RESULT 34

US-08-860-248C-25
; Sequence 25, Application US/08860248C
; Patent No. 6034056
; GENERAL INFORMATION:
; APPLICANT: DUTTA, Anand
; TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,248C
; FILING DATE: 24-JUNE-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426254.0
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505905.1
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9513904.4
; FILING DATE: 07-JUL-1995
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
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; LOCATION: 1
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US-08-860-248C-25

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 11dv 5
1111
DB 2 1LDV 5

RESULT 35
US-08-860-248C-26
; Sequence 26, Application US/08860248C
; Patent No. 6034056
; GENERAL INFORMATION:
; APPLICANT: DUTTA, Anand
; TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 122

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="N-ACETYL-2,4-DIAMINO-BUTYRIC ACID, D
US-08-860-248C-26

Query Match 78.3%; Score 18; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 11dv 5
1111
DB 2 1LDV 5

Search completed: June 10, 2002, 06:37:15
Job time: 38 sec

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L2 512 S EILDV/SQSP
L3 496 S L2 NOT L1
SAV L1 GAM251073A/A
SAV L3 GAM251073B/A

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0 S L1 OR L3

FILE 'HCAPLUS' ENTERED AT 08:02:59 ON 10 JUN 2002

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L6 351 S L3
L7 9 S EILDV
E LOBB R/AU
L8 113 S E3,E5,E7,E8
E BURKLY L/AU
L9 82 S E3-E6
E BIOGEN/PA,CS
L10 647 S E3-E56
L11 4 S L5-L7 AND L8-L10
L12 363 S L5-L7
L13 2 S L12 AND ?ASTHMA?
E ASTHMA/CT
E E3+ALL
L14 9231 S E2+NT
E E4+ALL
L15 6156 S E6,E5+NT
E E10+ALL
E E5+ALL
L16 8875 S E5,E4+NT
E E11+ALL
E E6+ALL
L17 681 S E4,E3+NT
L18 1 S L12 AND L14-L17
L19 35 S L12 AND (LUNG OR PULMON? OR AIRWAY OR AIR WAY OR BRONCH? OR R
L20 2 S L13,L18
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E E13+ALL
L21 38379 S E5,E4+NT
L22 944 S E36+NT-
E E38+ALL
L23 115430 S E4+NT
E E3+AKK
E E3+ALL
E E73+ALL
L24 700 S E2
E RESPIRATORY TRACT/CT
E E42+ALL
L25 177 S E1
E E2+ALL
L26 115430 S E4+NT
L27 18 S L12 AND L21-L26
L28 18 S L27 AND L19
L29 23 S L20,L28,L11
L30 16 S L19 NOT L29
L31 1 S L30 AND RESPIRATORY DISTRESS SYNDROME

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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L32 24 S L29,L31
L33 3 S L12 AND HYPERSENSITIV?
L34 3 S L12 AND ?ALLERG?
L35 5 S L33,L34
L36 1 S L35 AND L32
L37 4 S L35 NOT L32
L38 24 S L32,L36
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L40 1 S L39 AND L13,L18
L41 19 S L38 NOT L39
SEL DN 18
L42 1 S E1 AND L41
L43 2 S L40,L42
L44 4 S L11,L20 NOT L43
SEL HIT RN L43

FILE 'REGISTRY' ENTERED AT 08:23:14 ON 10 JUN 2002

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L46 9 S L45 AND L1-L3

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L47 53 S L1,L3
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L54 0 S L52 AND L53

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 08:26:10 ON 10 JUN 2002
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FILE COVERS 1907 - 10 Jun 2002 VOL 136 ISS 24
FILE LAST UPDATED: 7 Jun 2002 (20020607/ED)

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L43 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2002 ACS
AN 1999:505686 HCAPLUS
DN 131:139496

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TI Fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4
and for treating immunoinflammatory conditions
IN Arrhenius, Thomas S.; Elices, Mariano J.; Gaeta, Federico C. A.
PA Cytel Corporation, USA
SO U.S., 81 pp.
CODEN: USXXAM
DT Patent
LA English
IC ICM C07K005-08
NCL 530331000
CC 1-7 (Pharmacology)
Section cross-reference(s): 34, 63

FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5936065	A	19990810	US 1995-462424	19950605 <--
	CA 2177840	AA	19950615	CA 1994-2177840	19941205 <--
	CN 1142832	A	19970212	CN 1994-194969	19941205 <--
	US 5688913	A	19971118	US 1995-435286	19950505 <--
	US 6117840	A	20000912	US 1997-837154	19970414 <--
	US 6103870	A	20000815	US 1997-923026	19970903 <--
PRAI	US 1993-164101	B2	19931206	<--	
	US 1994-349024	B2	19941202		
	US 1995-435286	A1	19950505		
OS	MARPAT 131:139496				
AB	Peptidomimetic compds. are disclosed that inhibit the binding between the VLA-4 and the fibronectin CS-1 compd. Pharmaceutical compns. contg. a contemplated compd. and methods for treating immunoinflammatory conditions using the compd. are also disclosed.				
ST	fibronectin CS1 VLA4 binding inhibitor peptidomimetic; immunoinflammatory disease pharmaceutical peptidomimetic; inflammation inhibitor peptidomimetic				
IT	Cell adhesion molecules RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process) (ICAM-1 (intercellular adhesion mol. 1); fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)				
IT	Animal cell line (JURKAT; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)				
IT	Histocompatibility antigens RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process) (MHC (major histocompatibility complex), class II; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)				
IT	Cell adhesion molecules RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process) (VCAM-1; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)				
IT	Transplant and Transplantation Transplant and Transplantation (allotransplant, heart; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)				
IT	Heart (allotransplant; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)				
IT	Encephalomyelitis (autoimmune; fibronectin CS-1 peptidomimetics for inhibiting binding of				

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CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Artery
(coronary; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Allergy
(delayed hypersensitivity; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Immunity
(disorder; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Anti-inflammatory agents
 Antiasthmatics
 Antirheumatic agents
 Immunosuppressants
 Macrophage
 Peptidomimetics
 Rheumatoid arthritis
 Structure-activity relationship
 T cell (lymphocyte)
 (fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Fibronectins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Cell migration
(lymphocyte; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Drug delivery systems
(prodrugs; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Multiple sclerosis
(therapeutic agents; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Integrins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (.alpha.4.beta.1; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 125850-12-6 126235-03-8 150525-67-0 153982-81-1
184293-88-7 236100-96-2 236100-98-4 236100-99-5
236101-00-1 236101-01-2 236101-02-3
236101-03-4 236101-04-5 236101-05-6 236101-06-7
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
 (fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 7440-53-1D, Europium, complexes with peptidomimetics, biological studies
38763-90-5 77292-72-9 164740-10-7 177081-20-8 177081-48-0
177081-49-1 184293-89-8 184293-90-1 184293-91-2 184293-92-3
209600-74-8 209600-76-0 209600-77-1 209600-78-2 209600-79-3
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236100-89-3	236100-91-7	236100-94-0		

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 17186-57-1P 120125-44-2P 170986-07-9P

RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)

(prepn. and reaction; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 103-82-2, Phenylacetic acid, reactions 110-91-8, Morpholine, reactions 7536-58-5 13139-15-6 13734-34-4

RL: RCT (Reactant); RACT (Reactant or reagent)

(reaction; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Anon; EP 361977 1990 HCAPLUS
- (2) Anon; WO 91/03252 1991 HCAPLUS
- (3) Anon; WO 93/12809 1993 HCAPLUS
- (4) Eliccs, M; Cell Adhesion and Human Disease, Ciba Foundation Symposium 189 1995, P79
- (5) Furcht; US 5294511 1994 HCAPLUS
- (6) Ioria; J Med Chem 1991, V34, P2615
- (7) Komoriya, A; J Biol Chem 1991, V266, P15075 HCAPLUS
- (8) Mousa, S; Clin Pharm 1993, V83, P373
- (9) Mumford; US 5387504 1995 HCAPLUS
- (10) Nowlin, D; J Biol Chem 1993, V268, P20352 HCAPLUS
- (11) Pfaff, M; J Biol Chem 1994, V269, P20233 HCAPLUS
- (12) Snyderman; US 4822606 1989 HCAPLUS

L43 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2002 ACS

AN 1997:207658 HCAPLUS

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DN 126:199840
 TI Preparation of peptide derivatives as cell adhesion inhibitors
 IN Lin, Ko-Chung; Adams, Steven P.; Castro, Alfredo C.; Zimmerman, Craig N.; Cuervo, Julio Hernan; Lee, Wen-Cherng; Hammond, Charles E.; Carter, Mary Beth; Almquist, Ronald G.; Ensinger, Carol Lee
 PA Biogen, Inc., USA; Lin, Ko-Chung; Adams, Steven, P.; Castro, Alfredo, C.; Zimmerman, Craig, N.; Cuervo, Julio, Hernan; Lee, Wen-Cherng; Hammond, Charles, E.; Carter, Mary, Beth; et al.
 SO PCT Int. Appl., 117 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM C07K014-78
 ICS C07K005-02; C07K005-06; C07K005-08; C07K005-10; A61K038-04; A61K038-39
 CC 34-3 (Amino Acids, Peptides, and Proteins)
 Section cross-reference(s): 1, 63

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9703094	A1	19970130	WO 1996-US11570	19960711
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA				
US 6248713	B1	20010619	US 1995-498237	19950711
CA 2226868	AA	19970130	CA 1996-2226868	19960711
AU 9664894	A1	19970210	AU 1996-64894	19960711
AU 716276	B2	20000224		
EP 842196	A1	19980520	EP 1996-924444	19960711
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI				
CN 1193325	A	19980916	CN 1996-196380	19960711
BR 9609782	A	19990309	BR 1996-9782	19960711
JP 11511124	T2	19990928	JP 1996-505989	19960711
FI 9800033	A	19980305	FI 1998-33	19980109
NO 9800097	A	19980311	NO 1998-97	19980109
US 6239108	B1	20010529	US 1998-983391	19980810
PRAI US 1995-498237	A	19950711		
WO 1996-US11570	W	19960711		

OS MARPAT 126:199840

AB The present invention relates to novel peptide derivs. that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compds. and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compds. and pharmaceutical compn. of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases. Thus, coupling of 4-(2-MeC6H4NHCONH)C6H4CH2CO2H (prepn. given) with protected peptide H-Leu-Asp(OCH2Ph)-Val-OCH2Ph (prepn. given), followed by catalytic hydrogenolysis, gave cell adhesion inhibitor peptide 4-(2-MeC6H4NHCONH)C6H4CH2CO-Leu-Asp-Val-OH (I). All 408 prepd. peptide derivs., including I, inhibited VLA4-dependent adhesion to a bovine serum albumin conjugate with H-Cys-Tyr-Asp-Glu-Leu-Pro-Gln-Leu-Val-Thr-Leu-Pro-His-Pro-Asn-Leu-His-Gly-Pro-Glu-Ile-Leu-Asp-Val-Pro-Ser-Thr-OH, with IC50 values of <1 mM.

ST peptide prepn cell adhesion inhibitor; antiinflammatory drug peptide deriv prepn; autoimmune disease treatment peptide deriv prepn

IT Cell adhesion
 (inhibitors; prepn. of peptide derivs. as cell adhesion inhibitors)

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IT Anti-inflammatory drugs
Autoimmune diseases
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT Peptides, preparation
RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 187737-58-2P
RL: BAC (Biological activity or effector, except adverse); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of peptide derivs. as cell adhesion inhibitors)

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RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

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(prepn. of peptide derivs. as cell adhesion inhibitors)

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RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 187738-30-3DP, conjugate with bovine serum albumin

RL: BPR (Biological process); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)

(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 74-89-5, Methylamine, reactions 75-31-0, Isopropylamine, reactions 78-81-9, Isobutylamine 93-10-7, 2-Quinolinecarboxylic acid 95-55-6, 2-Hydroxyaniline 98-09-9, Phenylsulfonyl chloride 98-68-0, 4-Methoxybenzenesulfonyl chloride 98-98-6, Picolinic acid 100-46-9, Benzylamine, reactions 103-71-9, Phenyl isocyanate, reactions 103-80-0, Phenylacetyl chloride 108-91-8, Cyclohexylamine, reactions 110-89-4, Piperidine, reactions 110-91-8, Morpholine, reactions 348-54-9, 2-Fluoroaniline 501-52-0, Hydrocinnamic acid 501-97-3, 3-(4-Hydroxyphenyl)propionic acid 504-29-0, 2-Aminopyridine 614-68-6, o-Tolyl isocyanate 1197-55-3, 4-Aminophenylacetic acid 1603-40-3, 2-Amino-3-methylpyridine 2393-23-9, 4-Methoxybenzylamine 2462-31-9, Glycine benzyl ester hydrochloride 2577-48-2, Proline methyl ester 2620-50-0, Piperonylamine 2748-02-9 3373-59-9, Threonine methyl ester 3392-09-4 3392-12-9 3845-64-5 4070-48-8, Valine methyl ester 5081-36-7, 3-Methoxy-4-nitrobenzoic acid 6066-82-6, N-Hydroxysuccinimide 6624-49-3, 3-Isoquinolinecarboxylic acid 7531-52-4 7536-58-5 13139-15-6 13734-41-3 13798-75-9 15761-39-4 16013-85-7, 2,6-Dichloro-3-nitropyridine 16369-05-4, Valinol 18496-54-3, 4-Phenylbutyryl chloride 21760-98-5, Valine benzyl ester 33797-51-2,

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Eschenmoser's salt 38068-75-6 39552-81-3, Methyl p-aminophenylacetate
 41324-66-7, Proline benzyl ester 42726-73-8, tert-Butyl methyl malonate
 53308-95-5 53363-89-6 129460-09-9 135892-76-1

RL: RCT (Reactant)

(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 5803-22-5P 40851-91-0P 67579-92-4P, 3-Methoxy-4-nitrobenzoyl chloride
 90323-26-5P 136465-99-1P 153982-81-1P 181517-99-7P 181518-01-4P
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 187738-39-2P 187738-40-5P 187738-41-6P

RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation)

(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 38533-61-8P

RL: SPN (Synthetic preparation); PREP (Preparation)

(prepn. of peptide derivs. as cell adhesion inhibitors)

=> fil reg

FILE 'REGISTRY' ENTERED AT 08:26:18 ON 10 JUN 2002

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STRUCTURE FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5

DICTIONARY FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5

TSCA INFORMATION NOW CURRENT THROUGH January 7, 2002

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Crossover limits have been increased. See HELP CROSSOVER for details.

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 for more information. See STN Note 27, Searching Properties in the CAS
 Registry File, for complete details:

<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d sqide can tot 146

L46. ANSWER 1 OF 9 REGISTRY. COPYRIGHT 2002 ACS

RN 236101-05-6 REGISTRY

CN L-Proline, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-
 valyl- (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 6

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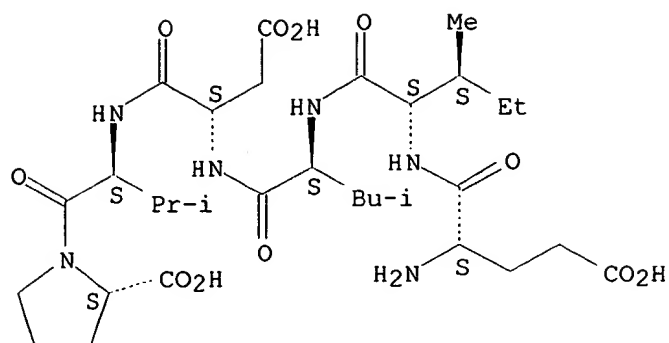
MF C31 H52 N6 O11

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

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1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 2 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN 236101-04-5 REGISTRY
CN L-Valine, L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-
aspartyl- (9CI) (CA INDEX NAME)
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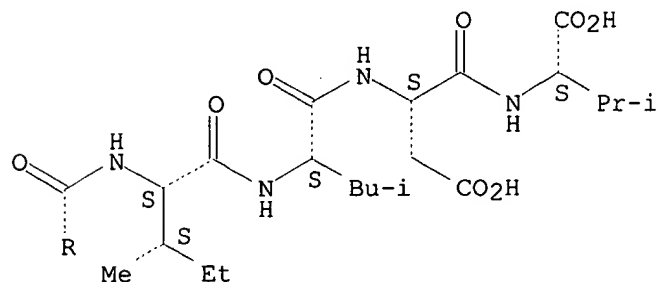
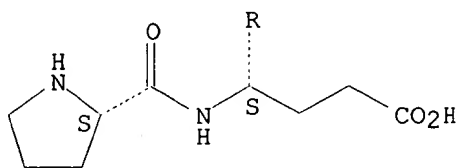
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MF C31 H52 N6 O11

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.



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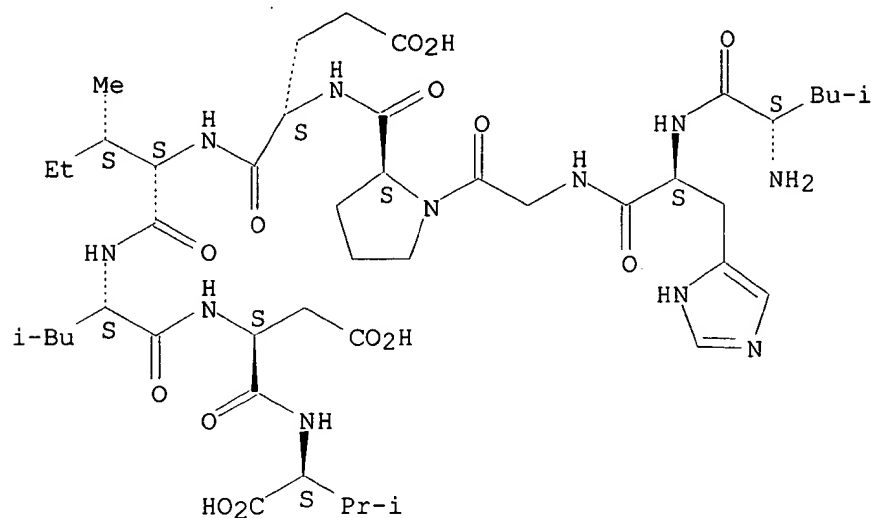
L46 ANSWER 3 OF 9 REGISTRY COPYRIGHT 2002 ACS
 RN 236101-02-3 REGISTRY
 CN L-Valine, L-leucyl-L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE; STEREOSEARCH
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HITS AT: 5-9
 MF C45 H73 N11 O14
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 LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 4 OF 9 REGISTRY COPYRIGHT 2002 ACS
 RN 236101-01-2 REGISTRY
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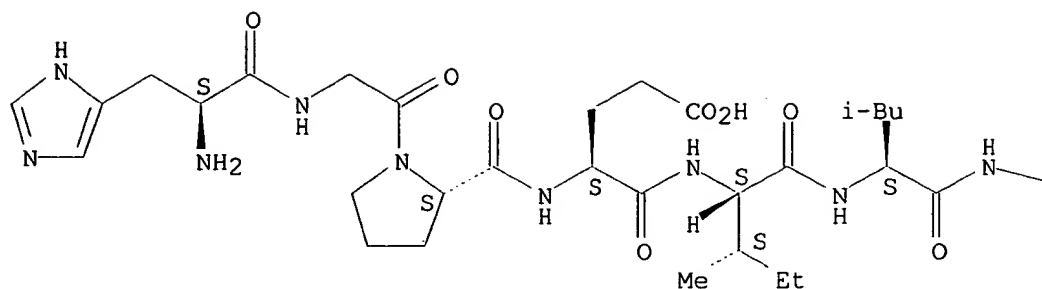
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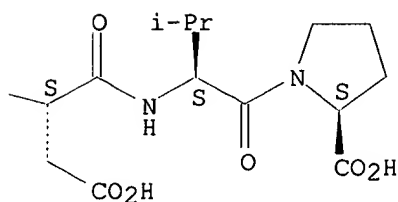
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PAGE 1-A



PAGE 1-B



1 REFERENCES IN FILE CA (1967 TO DATE)
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REFERENCE 1: 131:139496

L46 ANSWER 5 OF 9 REGISTRY COPYRIGHT 2002 ACS

RN 236101-00-1 REGISTRY

CN L-Serine, glycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl- (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

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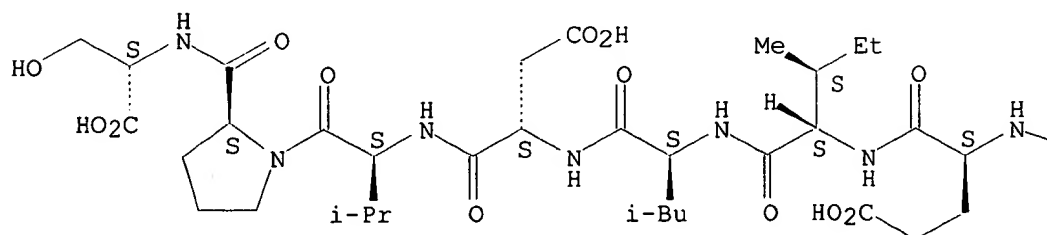
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SR CA

LC STN Files: CA, CAPLUS, USPATFULL

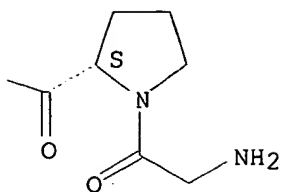
Absolute stereochemistry.

PAGE 1-A



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PAGE 1-B



1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 6 OF 9 REGISTRY COPYRIGHT 2002 ACS

RN 236100-99-5 REGISTRY

CN L-Valine, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl-L-threonyl- (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

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SEQ 1 EILDVPSTV

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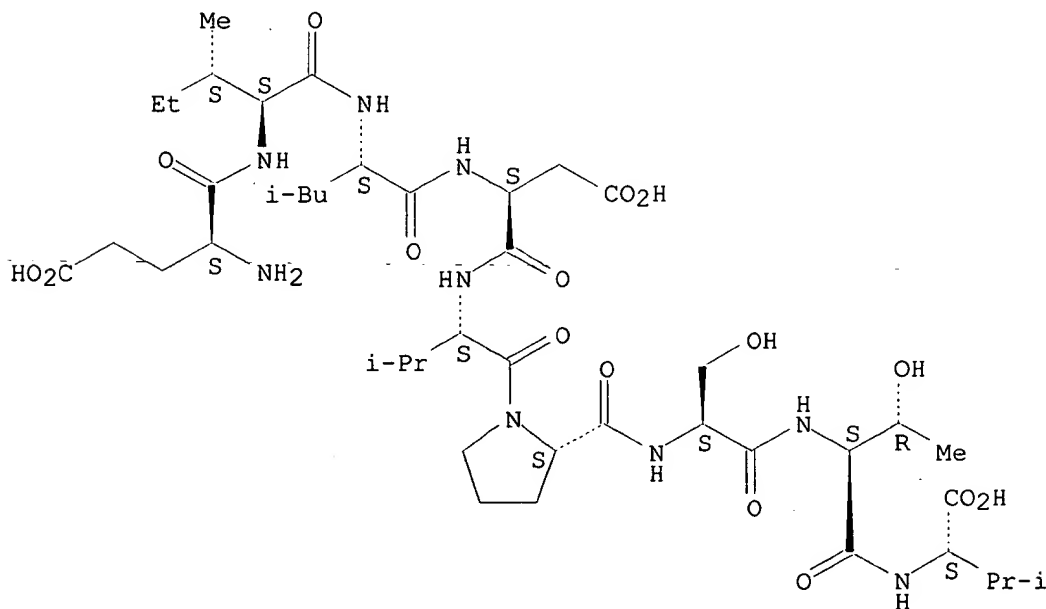
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MF C43 H73 N9 O16

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

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REFERENCE 1: 131:139496

L46 ANSWER 7 OF 9 REGISTRY COPYRIGHT 2002 ACS

RN 187738-30-3 REGISTRY

CN L-Threonine, L-cysteinyl-L-tyrosyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-leucyl-L-prolyl-L-glutamyl-L-leucyl-L-valyl-L-threonyl-L-leucyl-L-prolyl-L-histidyl-L-prolyl-L-asparaginy-L-leucyl-L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 4: PN: US6376538 SEQID: 4 unclaimed sequence

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 27

SEQ 1 CYDELPQLVT LPHPNLHGPE ILDPVST

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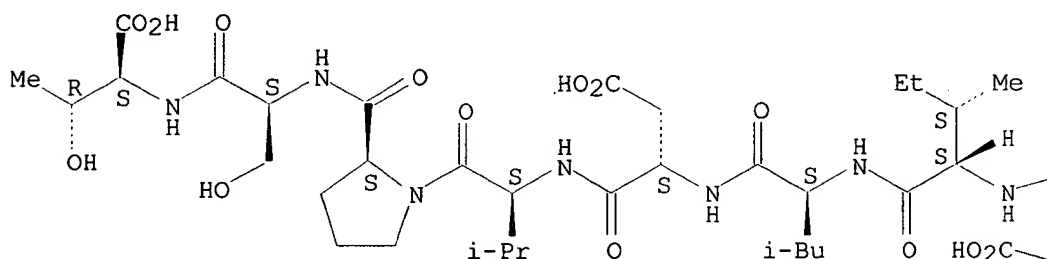
MF C135 H209 N33 O42 S

SR CA

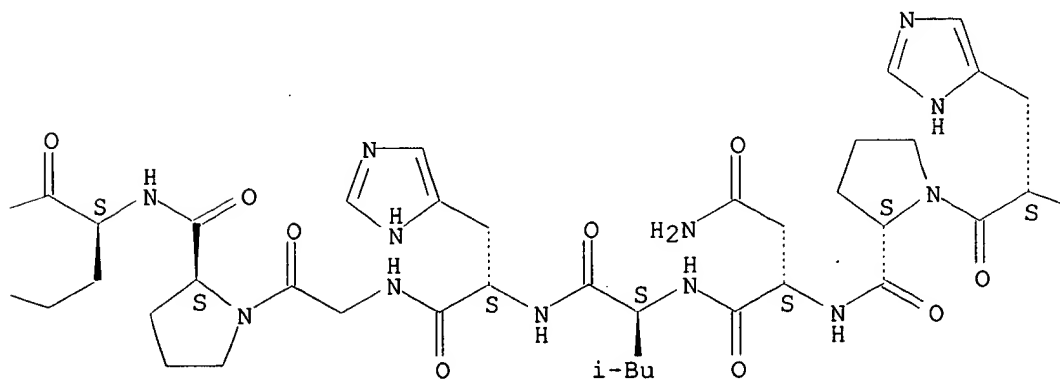
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A

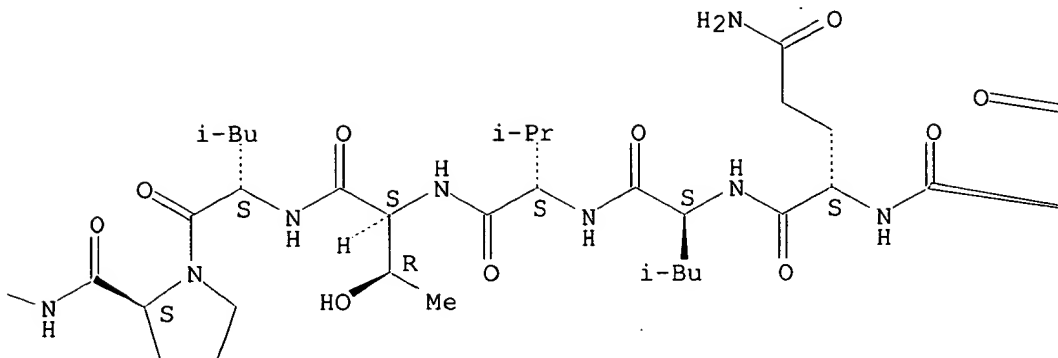


PAGE 1-B

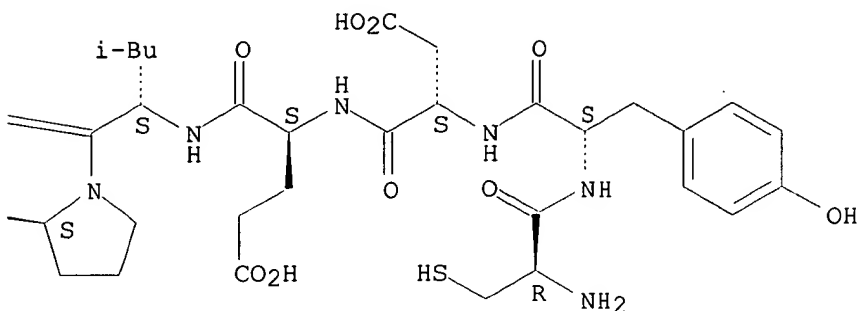


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PAGE 1-C



PAGE 1-D



2 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:325828

REFERENCE 2: 126:199840

L46 ANSWER 8 OF 9 REGISTRY COPYRIGHT 2002 ACS

RN 150525-67-0 REGISTRY

CN L-Valine, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-
 (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN L-Valine, N-[N-[N-(N-L-.alpha.-glutamyl-L-isoleucyl)-L-leucyl]-L-.alpha.-
 aspartyl]-

OTHER NAMES:

CN 23: PN: WO0004941 PAGE: 32 claimed sequence

CN 2: PN: US6376538 SEQID: 2 unclaimed sequence

CN 2: PN: WO0064474 PAGE: 19 unclaimed sequence

CN 457: PN: WO0069900 SEQID: 1142 unclaimed sequence

CN PN: US5962311 SEQID: 2 unclaimed sequence

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 5

SEQ 1 EILDV

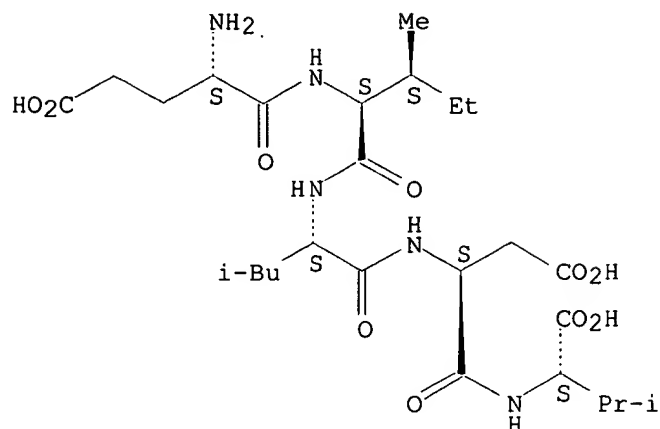
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HITS AT: 1-5

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MF C26 H45 N5 O10
 SR CA
 LC STN Files: CA, CAPLUS, CHEMCATS, TOXCENTER, USPATFULL

Absolute stereochemistry.



16 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 16 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:325828
 REFERENCE 2: 135:368937
 REFERENCE 3: 134:21425
 REFERENCE 4: 133:334056
 REFERENCE 5: 132:142003
 REFERENCE 6: 131:267956
 REFERENCE 7: 131:139496
 REFERENCE 8: 128:150383
 REFERENCE 9: 128:18371
 REFERENCE 10: 126:176918

L46 ANSWER 9 OF 9 REGISTRY COPYRIGHT 2002 ACS

RN 126235-03-8 REGISTRY

CN L-Threonine, glycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN L-Threonine, N-[N-[1-[N-[N-[N-[N-[N-(1-glycyl-L-prolyl)-L-.alpha.-glutamyl]-L-isoleucyl]-L-leucyl]-L-.alpha.-aspartyl]-L-valyl]-L-prolyl]-L-seryl]-

OTHER NAMES:

CN 24: PN: WO0192542 SEQID: 25 claimed sequence

FS PROTEIN SEQUENCE; STEREOSEARCH

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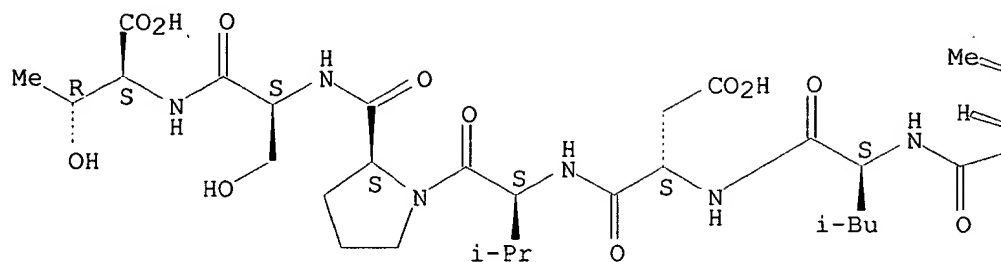
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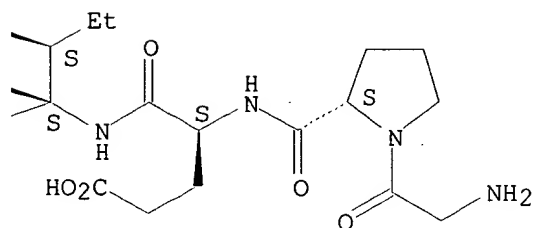
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 HITS AT: 3-7
 MF C45 H74 N10 O17
 SR CA
 LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



11 REFERENCES IN FILE CA (1967 TO DATE)
 11 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:32634
 REFERENCE 2: 131:139496
 REFERENCE 3: 130:163180
 REFERENCE 4: 129:245488
 REFERENCE 5: 126:14475
 REFERENCE 6: 120:215235
 REFERENCE 7: 119:201761
 REFERENCE 8: 115:270674
 REFERENCE 9: 115:254061
 REFERENCE 10: 115:229941

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 08:26:38 ON 10 JUN 2002
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FILE COVERS 1907 - 10 Jun 2002 VOL 136 ISS 24
FILE LAST UPDATED: 7 Jun 2002 (20020607/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

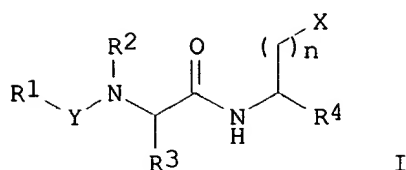
CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

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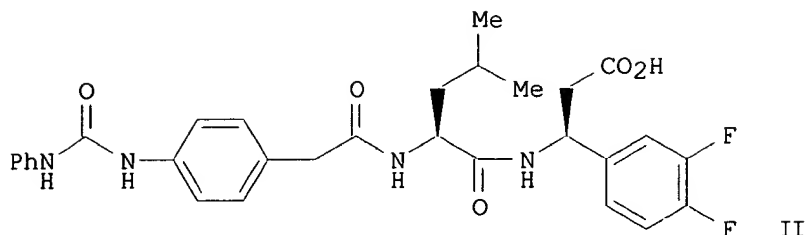
L44 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2002 ACS
AN 2002:312019 HCAPLUS
DN 136:325828
TI Preparation of dipeptide derivatives as cell adhesion inhibitors
IN Adams, Steven P.; Lin, Ko-Chung; Lee, Wen-Cherng; Castro, Alfredo C.; Zimmerman, Craig N.; Hammond, Charles E.; Liao, Yu-Sheng; Cuervo, Julio Hernan; Singh, Juswinder
PA **Biogen, Inc., USA**
SO U.S., 50 pp., Cont.-in-part of U.S. 6,306,840.
CODEN: USXXAM
DT Patent
LA English
IC ICM A61K031-357
ICS C07D317-46
NCL 514466000
CC 34-3 (Amino Acids, Peptides, and Proteins)
Section cross-reference(s): 1
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6376538	B1	20020423	US 1997-875321	19970919
	US 6306840	B1	20011023	US 1995-376372	19950123
	WO 9622966	A1	19960801	WO 1996-US1349	19960118
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE				
	EP 1142867	A2	20011010	EP 2001-107877	19960118
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI				
PRAI	US 1995-376372	A2	19950123		
	WO 1996-US1349	W	19960118		
	EP 1996-905316	A3	19960118		
OS	MARPAT 136:325828				
GI					

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I



II

AB Novel dipeptide analogs I [X = CO₂H, PO₃H⁻, SO₂R₅, SO₃H, OPO₃H⁻, CO₂R₄; Y = CO, SO₂, PO₂; n = 0-2; R₁ = optionally substituted alkyl, alkenyl, alkynyl, aryl-fused cycloalkyl, cycloalkenyl, aryl, aralkyl, aralkenyl, aralkynyl, alkoxy, alkenyloxy, aralkoxy, alkylamino, alkenylamino, alkynylamino, aryloxy, arylamino, N-alkylurea-substituted alkyl, heterocyclyl; R₂ = H, aryl, alkyl, alkenyl, alkynyl, cycloalkyl, cycloalkenyl, aralkyl; R₂NCR₃ = heterocyclic ring; R₃ = natural, unnatural, modified, or substituted amino acid side chain; R₄ = optionally substituted aryl, alkyl, cycloalkyl, alkenyl, cycloalkenyl, alkynyl, aralkyl, H, heterocyclyl, heterocyclylcarbonyl, aminocarbonyl, amido, alkylaminocarbonyl, arylaminocarbonyl, acylaminocarbonyl, acyl; R₅ = alkyl, alkenyl, alkynyl, cycloalkyl, cycloalkenyl, aryl, aralkyl, aralkenyl, aralkynyl] are prepd. as compds. useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compds. and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compds. and pharmaceutical compds. of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases. Thus, .beta.-amino acid-contg. dipeptide II, prepd. by std. methods, displayed an IC₅₀ of <50 nM in a cell adhesion inhibition assay.

ST cell adhesion inhibitor dipeptide analog prepn; aminoacyl amino acid prepn antiinflammatory

IT Anti-inflammatory agents

Cell adhesion

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT Dipeptides

RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 181518-22-9P 181521-43-7P

RL: PAC (Pharmacological activity); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion

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	181519-90-4P	181519-91-5P	181519-92-6P	181519-93-7P	181519-95-9P
	181519-97-1P	181519-98-2P	181520-00-3P	181520-01-4P	181520-03-6P
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RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU
(Therapeutic use); BIOL (Biological study); PREP (Preparation); USES
(Uses)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion
inhibitors)

IT	181523-62-6P	181523-63-7P	181523-65-9P	181523-67-1P	181523-68-2P
	181523-69-3P	181523-70-6P	181523-71-7P	181523-72-8P	181523-75-1P
	181523-77-3P	181523-78-4P	181525-84-8P	181525-85-9P	181525-86-0P
	181525-87-1P	181526-54-5P	181783-03-9P	181783-04-0P	

RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU
(Therapeutic use); BIOL (Biological study); PREP (Preparation); USES
(Uses)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion
inhibitors)

IT	52-90-4, L-Cysteine, reactions	60-32-2, 6-Aminohexanoic acid	65-45-2,
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Salicylamide 75-36-5, Acetyl chloride 96-50-4, 2-Aminothiazole 98-09-9, Phenylsulfonyl chloride 100-28-7, 4-Nitrophenyl isocyanate 103-71-9, Phenyl isocyanate, reactions 103-82-2, Phenylacetic acid, reactions 104-03-0, 4-Nitrophenylacetic acid 117-34-0, Diphenylacetic acid 122-78-1, Phenylacetaldehyde 123-90-0, Thiomorpholine 124-40-3, Dimethylamine, reactions 124-63-0, Methanesulfonyl chloride 140-10-3, (E)-Cinnamic acid, reactions 141-82-2, Malonic acid, reactions 150-13-0, 4-Aminobenzoic acid 156-38-7, 4-Hydroxyphenylacetic acid 372-09-8, Cyanoacetic acid 459-57-4, 4-Fluorobenzaldehyde 500-22-1, 3-Pyridinecarboxaldehyde 504-29-0, 2-Aminopyridine 581-96-4, 2-Naphthylacetic acid 614-68-6, 2-Methylphenyl isocyanate 621-29-4, 3-Methylphenyl isocyanate 624-83-9, Methyl isocyanate 643-28-7, 2-Isopropylaniline 700-87-8, 2-Methoxyphenyl isocyanate 768-56-9, 4-Phenyl-1-butene 771-50-6, Indole-3-carboxylic acid 943-89-5, 1011-54-7 1121-60-4, 2-Pyridinecarboxaldehyde 1189-71-5, Chlorosulfonyl isocyanate 1197-55-3, 4-Aminophenylacetic acid 1571-08-0, Methyl 4-formylbenzoate 3173-53-3, Cyclohexyl isocyanate 3320-86-3, 2-Nitrophenyl isocyanate 3392-09-4 3392-10-7 3397-35-1 3886-69-9, (R)-.alpha.-Methylbenzylamine 5068-28-0 5081-36-7, 3-Methoxy-4-nitrobenzoic acid 5292-21-7, Cyclohexylacetic acid 5678-48-8 5856-77-9, 2,2-Dimethylbutyryl chloride 6120-95-2, 1-Phenyl-1-cyclopropanecarboxylic acid 6335-76-8 14338-36-4, 3-Aminophenylacetic acid 14381-41-0 14381-42-1, 1-Indanecarboxylic acid 14737-89-4, (E)-3,4-Dimethoxycinnamic acid 14898-52-3, Benzenepropanoic acid, .beta.-amino-, Methyl ester 15100-75-1, Phenylalanine tert-butyl ester hydrochloride 16013-85-7, 2,6-Dichloro-3-nitropyridine 16947-80-1 17570-26-2, (E)-3-Methoxycinnamic acid 17859-70-0 18496-54-3, 4-Phenylbutyryl chloride 18598-74-8, Isoleucine methyl ester hydrochloride 19686-73-8, 1-Bromo-2-propanol 19947-39-8 26348-68-5 29668-44-8 30925-18-9 34036-07-2, 3,4-Difluorobenzaldehyde 34404-36-9 35000-38-5, tert-Butoxycarbonylmethylenetriphenylphosphorane 35161-71-8, N-Methylpropargylamine 38489-76-8, (E)-3,4-Methylenedioxycinnamic acid 39552-81-3, Methyl p-aminophenylacetate 39931-77-6, Ethyl 3-pyridylacetate 42726-73-8, tert-Butyl methyl malonate 60280-45-7 67579-92-4, 3-Methoxy-4-nitrobenzoyl chloride 71510-77-5 88950-64-5, 1-(tert-Butoxycarbonylamino)cyclopropanecarboxylic acid 128593-66-8 136465-99-1 149193-92-0 174579-31-8 181517-97-5 181517-98-6 181517-99-7 181518-00-3 181518-01-4 181518-02-5

RL: RCT (Reactant); RACT (Reactant or reagent)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 325-89-3P 3423-47-0P 3901-07-3P 5467-09-4P 6404-29-1P
 7042-36-6P, tert-Butyl (E)-cinnamate 30461-77-9P, Methyl
 (E)-3,4-dimethoxycinnamate 30914-88-6P 38533-61-8P 38693-90-2P
 39658-45-2P 40851-91-0P 40918-96-5P, Methyl (E)-3,4-
 methylenedioxycinnamate 40918-98-7P 53484-52-9P 56309-56-9P
 70232-19-8P 70232-20-1P 73158-83-5P 74405-07-5P 90323-26-5P
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181519-51-7P	181519-52-8P	181519-54-0P	181519-55-1P	181519-56-2P
181519-57-3P	181519-58-4P	181519-59-5P	181519-60-8P	181519-61-9P
181519-62-0P	181519-63-1P	181519-64-2P	181519-65-3P	181519-66-4P
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181519-72-2P	181519-73-3P	181519-75-5P	181519-76-6P	

RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 181519-89-1P

RL: SPN (Synthetic preparation); PREP (Preparation)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 136466-51-8 150525-67-0 187345-00-2

187738-30-3 414866-20-9

RL: PRP (Properties)

(unclaimed sequence; prepn. of dipeptide derivs. as cell adhesion inhibitors)

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L44 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2002 ACS

AN 2000:772477 HCAPLUS

DN 133:334056

TI Method for the treatment of fibrosis using an antagonist of the integrin alpha-4 subunit

IN Gotwals, Philip; Lobb, Roy R.

PA Biogen, Inc., USA

SO PCT Int. Appl., 59 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K039-395

ICS A61P011-00; A61P037-00

CC 15-3 (Immunochemistry)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000064474	A1	20001102	WO 2000-US10781	20000421
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1173201	A1	20020123	EP 2000-926238	20000421
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	BR 2000010669	A	20020219	BR 2000-10669	20000421
	NO 2001005122	A	20011221	NO 2001-5122	20011019
PRAI	US 1999-130847P	P	19990422		
	US 1999-137214P	P	19990601		
	WO 2000-US10781	W	20000421		
AB	Disclosed is a method of treating fibrosis in a human or animal subject. The method comprises administering to the subject an effective amt. of an antagonist, i.e. antibody, to VLA-4 integrin or fragment thereof.				
ST	fibrosis integrin alpha4 VLA4 antibody fragment				
IT	Integrins				
	RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)				
	(LPAM-1 (lymphocyte Peyer's patch high endothelial venule adhesion mol. 1); integrin .alpha.4 antibody or antagonist for treatment of fibrosis)				
IT	Nucleic acids				
	RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)				

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(anti-integrin .alpha.4 antibody-encoding; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Fusion proteins (chimeric proteins)
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antibody; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Body fluid
 (bronchoalveolar lavage fluid; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Lung, disease
 (fibrosis; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Immunoglobulins
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (fragments; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Animal
 Fibrosis
 Leukocyte
 (integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Antibodies
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Ligands
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (integrin .alpha.4; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Antibodies
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (monoclonal; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Integrins
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (.alpha.4; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT Integrins
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (.alpha.4.beta.1; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)

IT 304678-50-0
 RL: PRP (Properties)
 (Unclaimed; method for the treatment of fibrosis using an antagonist of the integrin alpha-4 subunit)

IT 136466-51-8 150525-67-0 187345-00-2
 RL: PRP (Properties)
 (unclaimed sequence; method for the treatment of fibrosis using an antagonist of the integrin alpha-4 subunit)

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L44 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2002 ACS

AN 2000:683175 HCAPLUS

DN 134:4000

TI Differential Induction of Gelatinase B (MMP-9) and Gelatinase A (MMP-2) in T Lymphocytes upon .alpha.4.beta.1-Mediated Adhesion to VCAM-1 and the CS-1 Peptide of Fibronectin

AU Yakubenko, Valentin P.; Lobb, Roy R.; Plow, Edward F.; Ugarova, Tatiana P.

CS Joseph J. Jacobs Center for Thrombosis and Vascular Biology, Department of Molecular Cardiology, Lerner Research Institute of the Cleveland Clinic Foundation, Cleveland, OH, 44195, USA

SO Experimental Cell Research (2000), 260, 73-84
CODEN: ECREAL; ISSN: 0014-4827

PB Academic Press

DT Journal

LA English

CC 15-10 (Immunochemistry)

AB Integrin .alpha.4.beta.1 on the surface of T lymphocytes interacts with vascular cell adhesion mol.-1 (VCAM-1) and fibronectin during migration of lymphocytes from the blood to sites of inflammation. Migrating lymphocytes actively modify their environment through a no. of mechanisms including proteolysis of the extracellular matrix by matrix metalloproteinases (MMP) synthesized by the cells. In this study, expression of MMP upon .alpha.4.beta.1-mediated adhesion of leukocytes to two major ligands, the IIIICS-1 domain of fibronectin and VCAM-1, has been examd. Adhesion of T lymphoblastoid Jurkat cells to the CS-1 peptide induced expression of mRNA for two MMPs, gelatinase A (MMP-2) and gelatinase B (MMP-9). As evaluated by relative RT-PCR and Northern blot analyses, the level of mRNA was upregulated about 4- to 5-fold for both MMPs compared to control cells maintained in suspension. With time, both enzymes were detected in conditioned media and inside the cells, and their identities were verified by Western blotting and gelatin zymog. Adhesion of Jurkat cells to the second major .alpha.4.beta.1 ligand, VCAM-1, upregulated mRNA for MMP-2 (3.5-fold) and failed to induce expression of mRNA for MMP-9. Accordingly, only MMP-2 protein was detected in conditioned media of cells adherent to VCAM-1. Occupancy of .alpha.4.beta.1 on the surface of suspended cells with sol. CS-1 peptide or VCAM-1 did not upregulate synthesis and release of MMPs. A similar pattern of induction of MMPs after adhesion to CS-1 and VCAM-1 was obsd. in T lymphocytes isolated from human blood. These results demonstrate that adhesion of T lymphocytes through .alpha.4.beta.1 to different ligands, which bind to similar or overlapping sites in the integrin, induces intracellular events leading to distinct patterns of MMPs biosynthesis. (c) 2000 Academic Press.

ST T lymphocyte adhesion integrin VCAM fibronectin gelatinase

IT Cell adhesion molecules

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(VCAM-1; differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT T cell (lymphocyte)

(adhesion; differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT Inflammation

Signal transduction, biological

(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT mRNA

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RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)

(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT Fibronectins

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT Integrins

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(.alpha.4.beta.1; differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT 107978-77-8

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT 146480-35-5, Gelatinase A 146480-36-6, Gelatinase B

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

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 AN 1999:216816 HCAPLUS
 DN 130:321465
 TI Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*
 AU Kalman, Sue; Mitchell, Wayne; Marathe, Rekha; Lammel, Claudia; Fan, Jun;
 Hyman, Richard W.; Olinger, Lynn; Grimwood, Jane; Davis, Ronald W.;
 Stephens, Richard S.
 CS Stanford DNA Sequencing and Technology, Center, Stanford University,
 Stanford, CA, 94305, USA
 SO Nature Genetics (1999), 21(4), 385-389
 CODEN: NGENEC; ISSN: 1061-4036
-
- PB Nature America
 DT Journal
 LA English
 CC 3-3 (Biochemical Genetics)
 Section cross-reference(s): 6, 7, 10
 AB *Chlamydia* are obligate intracellular eubacteria that are phylogenetically
 sepd. from other bacterial divisions. *C. trachomatis* and *C. pneumoniae*
 are both pathogens of humans but differ in their tissue tropism and
 spectrum of diseases. *C. pneumoniae* is a newly recognized species of
Chlamydia that is a natural pathogen of humans, and causes pneumonia and
 bronchitis. In the United States, approx. 10% of pneumonia cases and 5%
 of bronchitis cases are attributed to *C. pneumoniae* infection. Chronic
 disease may result following respiratory-acquired infection, such as
 reactive airway disease, adult-onset **asthma** and potentially lung
 cancer. In addn., *C. pneumoniae* infection has been assocd. with
 atherosclerosis. *C. trachomatis* infection causes trachoma, an ocular

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infection that leads to blindness, and sexually transmitted diseases such as pelvic inflammatory disease, chronic pelvic pain, ectopic pregnancy and epididymitis. Although relatively little is known about *C. trachomatis* biol., even less is known concerning *C. pneumoniae*. Comparison of the *C. pneumoniae* genome with the *C. trachomatis* genome will provide an understanding of the common biol. processes required for infection and survival in mammalian cells. Genomic differences are implicated in the unique properties that differentiate the two species in disease spectrum. Anal. of the 1,230,230-nt *C. pneumoniae* genome revealed 214 protein-coding sequences not found in *C. trachomatis*, most without homologues to other known sequences. Prominent comparative findings include expansion of a novel family of 21 sequence-variant outer-membrane proteins, conservation of a type-III secretion virulence system, three serine/threonine protein kinases and a pair of paralogous phospholipase-D-like proteins, addnl. purine and biotin biosynthetic capability, a homolog for arom. amino acid (tryptophan) hydroxylase and the loss of tryptophan biosynthesis genes.

- ST sequence Chlamydia pneumoniae genome; species difference Chlamydia trachomatis pneumoniae genome sequence comparison
- IT Proteins, specific or class
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Pmp (polymorphic membrane protein); comparative genomes of Chlamydia pneumoniae and *C. trachomatis*)
- IT Chlamydia trachomatis
Genome
(comparative genomes of Chlamydia pneumoniae and *C. trachomatis*)
- IT Chlamydia pneumoniae
(genomic sequence of; comparative genomes of Chlamydia pneumoniae and *C. trachomatis*)
- IT DNA sequences
Protein sequences
(of Chlamydia pneumoniae)
- IT Gene, microbial
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(pmp; comparative genomes of Chlamydia pneumoniae and *C. trachomatis*)
- IT 75432-95-0, Arom. amino acid oxidase
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(*C. pneumoniae* gene for; comparative genomes of Chlamydia pneumoniae and *C. trachomatis*)
- IT 135946-71-3, Protein MOMP (Chlamydia pneumoniae strain IOL-207 precursor reduced) 136363-37-6, Protein (Chlamydia pneumoniae clone pLC3 71.5-kilodalton reduced) 145170-64-5, Chaperonin 10 (Chlamydia pneumoniae strain AR-39 gene groES) 172279-76-4 172313-16-5
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 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
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 (amino acid sequence; comparative genomes of Chlamydia pneumoniae and
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 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)

(amino acid sequence; comparative genomes of Chlamydia pneumoniae and
 C. trachomatis)

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 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; comparative genomes of Chlamydia pneumoniae and
 C. trachomatis)
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; comparative genomes of Chlamydia pneumoniae and
C. trachomatis)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; comparative genomes of Chlamydia pneumoniae and
C. trachomatis)

IT	223700-98-9	223703-35-3	223728-83-4	223728-84-5	223728-85-6
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223729-71-3	223729-72-4	223729-73-5	223729-74-6	223729-75-7
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; comparative genomes of *Chlamydia pneumoniae* and
C. trachomatis)

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

- (1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 HCAPLUS
- (2) Campbell, L; J Clin Microbiol 1987, V25, P1911 HCAPLUS
- (3) Emre, U; J Infect Dis 1995, V172, P265 MEDLINE
- (4) Fong, I; J Clin Microbiol 1997, V35, P48 MEDLINE
- (5) Grayston, J; Int J Syst Bacteriol 1989, V39, P88
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- (7) Kuo, C; Arterioscler Thromb 1993, V13, P1501 MEDLINE
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- (10) Kuo, C; Proc Natl Acad Sci USA 1995, V92, P6911 HCAPLUS
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Chlamydial Infection 1998, P543
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- (19) Salzberg, S; Nucleic Acids Res 1997, V26, P544
- (20) Schachter, J; West J Med 1990, V153, P523 MEDLINE
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- (22) Stephens, R; Science 1998, V282, P754 HCAPLUS
- (23) Thompson, J; Nucleic Acids Res 1994, V22, P4673 HCAPLUS

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E11 THROUGH E16 ASSIGNED

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STRUCTURE FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5

DICTIONARY FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5

TSCA INFORMATION NOW CURRENT THROUGH January 7, 2002

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS

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Registry File, for complete details:

<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d sqide can tot

L56 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 223737-50-6 REGISTRY

CN L-Lysine, L-methionyl-L-.alpha.-aspartyl-L-leucyl-L-glutaminy-L-alanyl-L-phenylalanyl-L-.alpha.-glutamyl-L-iso-leucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-glutaminyglycyl-L-methionyl-L-leucyl-L-threonyl-L-.alpha.-aspartyl-L-glutaminy-L-arginyl-L-lysyl-L-histidyl-L-iso-leucyl-L-glutaminy-L-methionyl-L-leucyl-L-histidyl-L-lysyl-L-histidyl-L-asparaginy-L-seryl-L-iso-leucyl-L-.alpha.-glutamyl-L-iso-leucyl-L-phenylalanyl-L-leucyl-L-seryl-L-asparaginy-L-methionyl-L-valyl-L-valyl-L-.alpha.-glutamyl-L-valyl-L-lysyl-L-leucyl-L-phenylalanyl-L-phenylalanyl-L-lysyl-L-threonyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AE001651-derived protein GI 4376987

CN GenBank AP002547-derived protein GI 8979057

CN Protein (Chlamydia pneumoniae gene CPn0685)

CN Protein (Chlamydia pneumoniae strain J138 gene CPj0685)

FS PROTEIN SEQUENCE

SQL 50

SEQ 1 MDLQAFEILD VQGLTDQRK HIQMLHKHNS IEIFLSNMVV EVKLFFKTLK

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HITS AT: 7-11

MF C270 H436 N70 O73 S4

CI MAN

SR CA

LC STN Files: CA, CAPLUS

2 REFERENCES IN FILE CA (1967 TO DATE)

2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 134:232463

REFERENCE 2: 130:321465

L56 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 223710-22-3 REGISTRY

CN Synthetase, methionyl-transfer ribonucleate (Chlamydia pneumoniae gene metG) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AE001598-derived protein GI 4376385

CN Methionyl-tRNA synthetase (Chlamydia pneumoniae gene metG)

FS PROTEIN SEQUENCE

SQL 551

SEQ 1 MPQKVLITSA LPYANGPLHF GHIAGVYLPA DVYARFRLL GDDVLYICGS
51 DEFGIAITLN ADREGLGYQE YVDMYHKLHK DTFEKLGFAL DFFSRTTNPF
101 HAEVLQDFYS QLKASGLIEN RISEQLYSEQ EQRFLADRYV EGTCPRCGFD
151 HARGDECQSC GADYEAIDLI GPKSKISGVE LVKKETEHSY FLLDRMKDAL
201 LSFIQGCYLP DHVRKFVVDY IEHVRRAIT RDLSWGIPVP DFPQKVIFYVW
251 FDAPIGYISG TMEWAASQGN PDEWKRFWLE DGVEYVQFIG KDNLPFHSHV
301 FPAMELGQKL DYKKVDALVV SEFYLLGRQ FSKSEGNVVD MDKFLSSYSL
351 DKLRVLAAT APETSDSEFT FLDFKTRCNS ELVGKFGNFI NRVLAFAEKN
401 HYDKLSYHSV VLESDRAFL EEARQLVRDA EKCYPEYSLR KATSVIMSLA
451 ALGNVYFNQQ APWKLLKEGT RERVEAILFC ACYCQKLLAL ISYPIIPESA
501 VAIWEMISPK SLENCNLDTM YARDLWKEEI LDVINEEFHL KSPRLLFSTTV

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551 E

HITS AT: 529-533

MF Unspecified

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 LC STN Files: CA, CAPLUS
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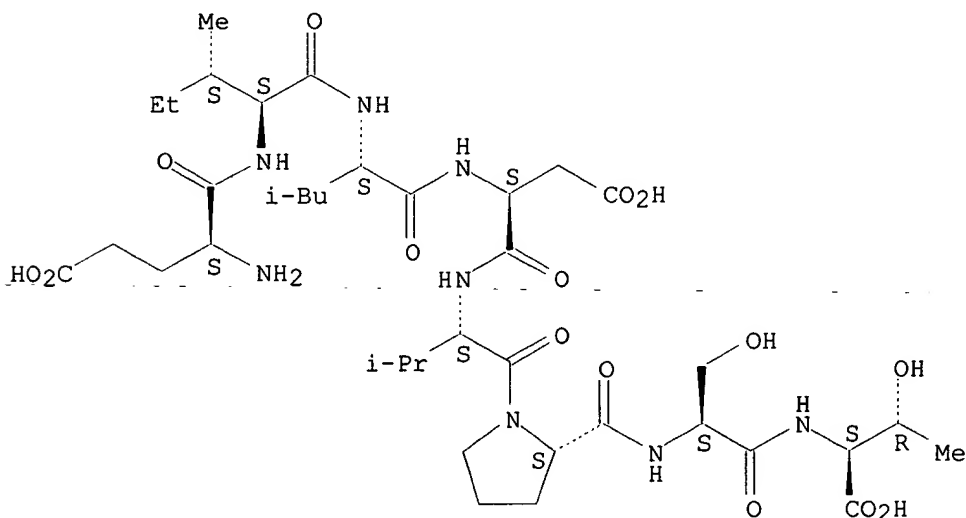
L56 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2002 ACS
 RN 136466-51-8 REGISTRY
 CN L-Threonine, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)
 OTHER CA INDEX NAMES:
 CN L-Threonine, N-[N-[1-[N-[N-[N-(N-L-.alpha.-glutamyl-L-isoleucyl)-L-leucyl]-L-.alpha.-aspartyl]-L-valyl]-L-prolyl]-L-seryl]-
 OTHER NAMES:
 CN 1: PN: US6376538 SEQID: 1 unclaimed sequence
 CN 1: PN: WO0064474 PAGE: 19 unclaimed sequence
 CN 24: PN: WO0004941 PAGE: 32 claimed sequence
 CN 458: PN: WO0069900 SEQID: 1143 unclaimed sequence
 CN 47: PN: US6051429 SEQID: 48 unclaimed sequence
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 8

SEQ 1 EILDVPST

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HITS AT: 1-5
 MF C38 H64 N8 O15
 CI COM
 SR CA
 LC STN Files: CA, CAPLUS, CHEMCATS, TOXCENTER, USPATFULL

Absolute stereochemistry.



17 REFERENCES IN FILE CA (1967 TO DATE)
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 17 REFERENCES IN FILE CAPLUS (1967 TO DATE)

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REFERENCE 2: 136:325828
REFERENCE 3: 134:21425
REFERENCE 4: 133:334056
REFERENCE 5: 133:221490
REFERENCE 6: 132:289590
REFERENCE 7: 132:142003
REFERENCE 8: 131:175085
REFERENCE 9: 131:175083
REFERENCE 10: 130:48275

L56 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 107978-77-8 REGISTRY

CN L-Threonine, L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-leucyl-L-prolyl-L-glutamyl-L-leucyl-L-valyl-L-threonyl-L-leucyl-L-prolyl-L-histidyl-L-prolyl-L-asparaginyl-L-leucyl-L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 15: PN: US6013628 SEQID: 15 claimed protein
CN 37: PN: US6051429 SEQID: 17 unclaimed sequence
CN 3: PN: US20020012942 SEQID: 3 claimed protein
CN 3: PN: WO0187071 SEQID: 4 unclaimed sequence
CN 4: PN: US20020012942 SEQID: 4 claimed protein
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 25

SEQ 1 DELPQLVTLP HPNLHGPEIL DVPST
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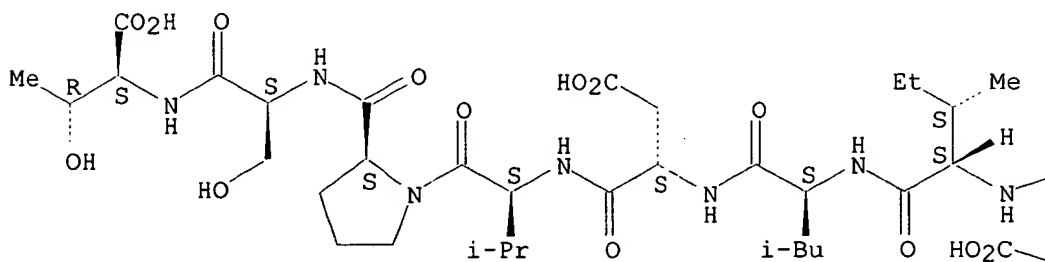
MF C123 H195 N31 O39

SR CA

LC STN Files: CA, CANCERLIT, CAPLUS, CHEMCATS, MEDLINE, TOXCENTER,
USPATFULL

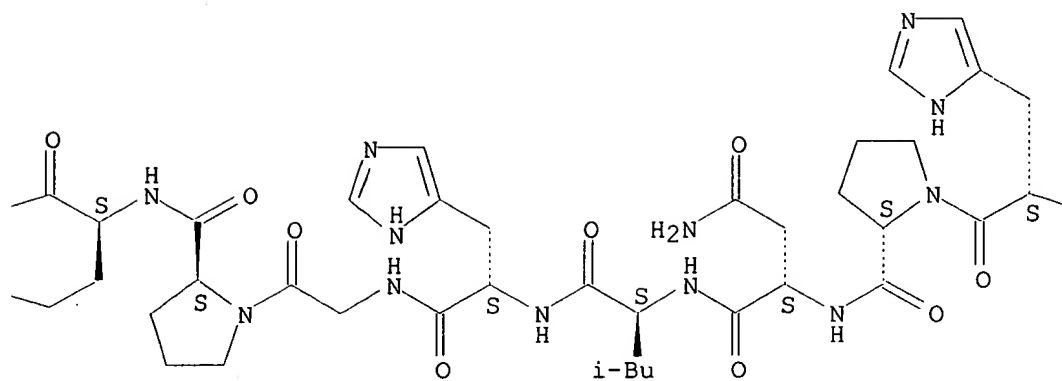
Absolute stereochemistry.

PAGE 1-A

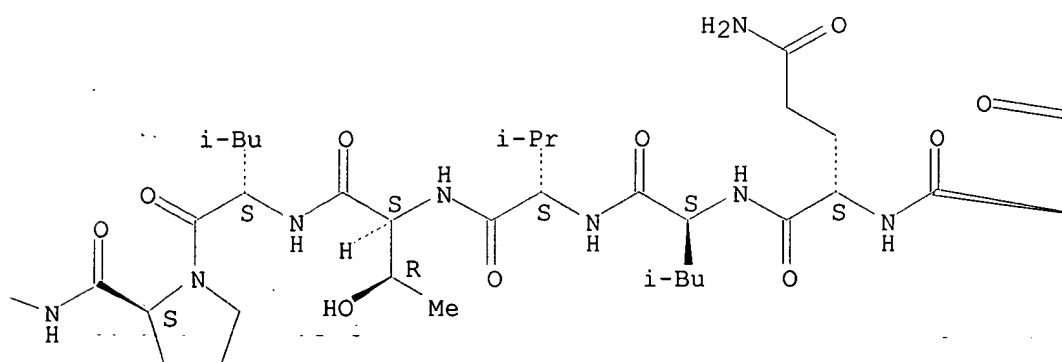


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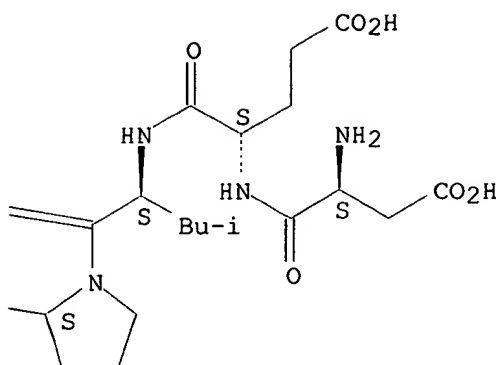


PAGE 1-C



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PAGE 1-D



32 REFERENCES IN FILE CA (1967 TO DATE)
3 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
32 REFERENCES IN FILE CAPLUS (1967 TO DATE)

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REFERENCE	4:	134:4000
REFERENCE	5:	133:261094
REFERENCE	6:	132:289590
REFERENCE	7:	132:88194
REFERENCE	8:	131:175085
REFERENCE	9:	131:175083
REFERENCE	10:	131:125484

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CA INDEXING COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)
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FILE 'USPAT2' ENTERED AT 08:27:50 ON 10 JUN 2002
CA INDEXING COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)

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L50  ANSWER 1 OF 13  USPATFULL
AN    2002:88519  USPATFULL
TI    Cell adhesion inhibitors
IN    Adams, Steven P., Andover, MA, United States
      Lin, Ko-Chung, Lexington, MA, United States
      Lee, Wen-Cherng, Lexington, MA, United States
      Castro, Alfredo C., Woburn, MA, United States
      Zimmerman, Craig N., Somerville, MA, United States
      Hammond, Charles E., Burlington, MA, United States
      Liao, Yu-Sheng, Lexington, MA, United States
      Cuervo, Julio Hernan, Arlington, MA, United States
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Singh, Juswinder, Malden, MA, United States
PA Biogen, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6376538 B1 20020423
WO 9622966 19960801
AI US 1997-875321 19970919 (8)
WO 1996-US1349 19960118
19970919 PCT 371 date
RLI Continuation-in-part of Ser. No. US 1995-376372, filed on 23 Jan 1995,
now patented, Pat. No. US 6306840
DT Utility
FS GRANTED
EXNAM Primary Examiner: Aulakh, Charanjit S.
LREP Fish & Richardson P.C.
CLMN Number of Claims: 56
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 4655

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel compounds that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compounds and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compounds and pharmaceutical compositions of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 136466-51-8 150525-67-0 187738-30-3
(unclaimed sequence; prepn. of dipeptide derivs. as cell adhesion inhibitors)

L50 ANSWER 2 OF 13 USPATFULL

AN 2002:84902 USPATFULL
TI Nucleic acids, proteins and antibodies
IN Rosen, Craig A., Laytonsville, MD, UNITED STATES
Ruben, Steven M., Olney, MD, UNITED STATES
PI US 2002044941 A1 20020418
AI US 2001-925302 A1 20010810 (9)
RLI Continuation-in-part of Ser. No. WO 2000-US5918, filed on 8 Mar 2000,
UNKNOWN
PRAI US 1999-124270P 19990312 (60)
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 21121

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel lung cancer related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "lung cancer antigens," and antibodies that immunospecifically bind these polypeptides, and the use of such lung cancer polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the lung, including, but not limited to, the presence of lung cancer and lung cancer metastases. More specifically, isolated lung cancer nucleic acid molecules are provided encoding novel lung cancer polypeptides. Novel lung cancer polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human lung cancer polynucleotides, polypeptides, and/or antibodies. The invention further relates to

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diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the lung, including lung cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compositions for inhibiting or promoting the production and/or function of the polypeptides of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 409148-95-4P

(amino acid sequence; human nucleic acids and their encoded proteins and antibodies assocd. with lung cancer)

L50 ANSWER 3 OF 13 USPATFULL

AN 2002:78727 USPATFULL

TI INTEGRIN-TARGETING VECTORS HAVING TRANSFECTION ACTIVITY

IN HART, STEPHEN L., LONDON, UNITED KINGDOM

PI US 2002042384 A1 20020411

AI US 1999-424656 A1 19991129 (9)

WO 1998-GB1577 19980529

PRAI GB 1997-11115 19970529

DT Utility

FS APPLICATION

LREP NIXON & VANDERHYE, 1100 NORTH GLEBE ROAD, 8TH FLOOR, ARLINGTON, VA, 222014714

CLMN Number of Claims: 55

ECL Exemplary Claim: 1

DRWN 9 Drawing Page(s)

LN.CNT 1527

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A complex that comprises (i) a nucleic acid, (ii) an integrin-binding component, for example, an integrin-binding peptide, (iii) a polycationic nucleic acid-binding component, for example, oligolysine, and (iv) a lipid component, for example, a cationic liposome, has transfection activity.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 216964-48-6

(integrin-targeting vectors having transfection activity)

L50 ANSWER 4 OF 13 USPATFULL

AN 2001:93479 USPATFULL

TI Cell adhesion inhibitors

IN Lin, Ko-Chung, Lexington, MA, United States

Adams, Steven P., Andover, MA, United States

Castro, Alfredo C., Woburn, MA, United States

Zimmerman, Craig N., Somerville, MA, United States

Cuervo, Julio Hernan, Cambridge, MA, United States

Lee, Wen-Cherng, Lexington, MA, United States

Hammond, Charles E., Burlington, MA, United States

Carter, Mary Beth, Belmont, MA, United States

Almquist, Ronald G., Lexington, MA, United States

PA Biogen, Inc., Cambridge, MA, United States (U.S. corporation)

PI US 6248713 B1 20010619

AI US 1995-498237 19950711 (8)

DT Utility

FS GRANTED

EXNAM Primary Examiner: Celsa, Bennett

LREP Fish & Richardson P.C.

CLMN Number of Claims: 13

ECL Exemplary Claim: 1

DRWN No Drawings

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LN.CNT 2501

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel compounds that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compounds and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compounds and pharmaceutical compositions of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 187738-30-3DP, conjugate with bovine serum albumin
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 187738-30-3P
(prepn. of peptide derivs. as cell adhesion inhibitors)

L50 ANSWER 5 OF 13 USPATFULL

AN 2001:79133 USPATFULL

TI Cell adhesion inhibitors

IN Lin, Ko-Chung, Lexington, MA, United States
Adams, Steven P., Andover, MA, United States
Castro, Alfredo C., Woburn, MA, United States
Zimmerman, Craig N., Topsfield, MA, United States
Cuervo, Julio Hernan, Arlington, MA, United States
Lee, Wen-Cherng, Lexington, MA, United States
Hammond, Charles E., Burlington, MA, United States
Carter, Mary Beth, Belmont, MA, United States
Almquist, Ronald G., Lexington, MA, United States
PA Biogen, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6239108 B1 20010529
WO 9703094 19970130
AI US 1998-983391 19980810 (8)
WO 1996-US11570 19960711
19980810 PCT 371 date
19980810 PCT 102(e) date

DT Utility

FS Granted

EXNAM Primary Examiner: Davenport, Avis M.

LREP Fish & Richardson P.C.

CLMN Number of Claims: 49

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 3146

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel compounds that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compounds and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compounds and pharmaceutical compositions of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 187738-30-3DP, conjugate with bovine serum albumin
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 187738-30-3P
(prepn. of peptide derivs. as cell adhesion inhibitors)

L50 ANSWER 6 OF 13 USPATFULL

AN 2000:98458 USPATFULL

TI Compounds that inhibit the binding of integrins to their receptors

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IN Scott, Ian L., Albany, NY, United States
 Raju, Bore G., Fremont, CA, United States
 Biediger, Ronald J., Houston, TX, United States
 Grabbe, Vanessa O., Sugar Land, TX, United States
 Kassir, Jamal, Houston, TX, United States
 Keller, Karin M., Houston, TX, United States
 Kogan, deceased, Timothy P., late of Sugar Land, TX, United States by
 Patricia Woodard Kogan, executrix
 Lin, Shuqun, Huntingdon Valley, PA, United States
 Market, Robert V., Pearland, TX, United States
 PA Texas Biotechnology Corporation, Inc., Houston, TX, United States (U.S.
 corporation)
 PI US 6096773 20000801
 AI US 1999-292459 19990415 (9)
 PRAI US 1998-82019P 19980416 (60)
 DT Utility
 FS Granted
 EXNAM Primary Examiner: McKane, Joseph K.; Assistant Examiner: Solola, Taofiq
 A.
 LREP Rockey, Milnamow & Katz, Ltd.
 CLMN Number of Claims: 10
 ECL Exemplary Claim: 1
 DRWN No Drawings
 LN.CNT 1469

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A method for the inhibition of the binding of .alpha..sub.4 .beta..sub.1
 integrin to its receptors, for example VCAM-1 (vascular cell adhesion
 molecule-1) and fibronectin; compounds that inhibit this binding;
 pharmaceutically active compositions comprising such compounds; and the
 use of such compounds either as above, or in formulations for the
 control or prevention of diseases states in which .alpha..sub.4
 .beta..sub.1 is involved.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 247094-59-3
 (ovalbumin conjugates; compds. that inhibit binding of integrins to
 receptors such as VCAM-1 and fibronectin)

L50 ANSWER 7 OF 13 USPATFULL
 AN 2000:27952 USPATFULL
 TI Fibronectin adhesion inhibitors
 IN Dutta, Anand Swaroop, Macclesfield, United Kingdom
 PA Zeneca Limited, London, United Kingdom (non-U.S. corporation)
 PI US 6034056 20000307
 WO 9620216 19960704
 AI US 1997-860248 19970624 (8)
 WO 1995-GB2992 19951221
 19970624 PCT 371 date
 19970624 PCT 102(e) date
 PRAI GB 1994-26254 19941224
 GB 1995-5905 19950324
 GB 1995-13904 19950707
 DT Utility
 FS Granted
 EXNAM Primary Examiner: Tsang, Cecilia J.
 LREP Phillsbury Madison & Sutro, LLP Intellectual Property Group
 CLMN Number of Claims: 12
 ECL Exemplary Claim: 1
 DRWN 16 Drawing Figure(s); 22 Drawing Page(s)
 LN.CNT 3750

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Cyclic peptides of formula (1): ##STR1## Wherein: AA1 is an L or D amino
 acid selected from Ile and Leu or amino acid analogue thereof; AA2 is an

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L amino acid selected from Leu or amino acids analogue thereof; AA3 is an L amino acid selected from Asp or amino acid analogue thereof containing a carboxy group in its side chain; AA4 is an L amino acid selected from Val or amino acid analogue thereof and; LINKER represents a linking moiety for linking N terminus of AA1 to C terminus of AA4 to form a cyclic peptide containing a heterocyclic ring having 17 to 30 members. The cyclic peptides inhibit the interaction of vascular cell adhesion molecule-1 and fibronectin with integrin very late antigen 4 and have therapeutic applications such as in rheumatoid arthritis or multiple sclerosis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 180575-30-8P 180575-31-9P 180575-32-0P
180575-33-1P

(prepn. of cyclopeptide fibronectin adhesion inhibitors for treatment of rheumatoid arthritis and multiple sclerosis)

L50 ANSWER 8 OF 13 USPATFULL

AN 1999:163664 USPATFULL

TI Inhibitors of leukocyte adhesion

IN Thorsett, Eugene D., Moss Beach, CA, United States

Yednock, Theodore A., Fairfax, CA, United States

Pleiss, Michael A., Fremont, CA, United States

PA Elan Pharmaceuticals, Inc., South San Francisco, CA, United States (U.S. corporation)

PI US 6001809 19991214

AI US 1995-467580 19950606 (8)

RLI Continuation-in-part of Ser. No. US 1994-273055, filed on 11 Jul 1994, now abandoned

DT Utility

FS Granted

EXNAM Primary Examiner: Tsang, Cecilia J.; Assistant Examiner: Delacroix-Muirheid, C.

LREP Stratford, Carol A., Duvall, Jean M. Burns, Doane, Swecker & Mathis, LLP

CLMN Number of Claims: 13

ECL Exemplary Claim: 1

DRWN 2 Drawing Figure(s); 1 Drawing Page(s)

LN.CNT 2132

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides peptides which block cellular adhesion mediated by VLA-4. The peptides can be used to treat a number of inflammatory diseases, in particular, inflammatory brain disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 174962-82-4 174962-83-5

(anti-inflammatory peptide inhibitors of leukocyte adhesion mediated by VLA-4)

L50 ANSWER 9 OF 13 USPATFULL

AN 1999:92778 USPATFULL

TI CS-1 peptidomimetics, compositions and methods of using the same

IN Arrhenius, Thomas S., San Diego, CA, United States

Elices, Mariano J., San Diego, CA, United States

Gaeta, Federico C. A., Olivenhain, CA, United States

PA Cytel Corporation, San Diego, CA, United States (U.S. corporation)

PI US 5936065 19990810

AI US 1995-462424 19950605 (8)

RLI Continuation-in-part of Ser. No. US 1994-349024, filed on 2 Dec 1994, now abandoned which is a continuation-in-part of Ser. No. US 1993-164101, filed on 6 Dec 1993, now abandoned

DT Utility

FS Granted

EXNAM Primary Examiner: Tsang, Cecilia J.; Assistant Examiner: Lukton, David

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LREP Campbell & Flores LLP
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 3625

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention contemplates a compound defined by the following formula: ##STR1## that inhibits the binding between the VLA-4 and the fibronectin CS-1 compound. Pharmaceutical compositions containing a contemplated compound and methods for treating immunoinflammatory conditions using the compound are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 126235-03-8 150525-67-0 236100-99-5
236101-00-1 236101-01-2 236101-02-3
236101-04-5 236101-05-6
(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

L50 ANSWER 10 OF 13 USPATFULL

AN 1999:19112 USPATFULL
TI Cyclic CS-1 peptidomimetics, compositions and methods of using same
IN Arrhenius, Thomas S., San Diego, CA, United States
Tempczyk, Anna, San Diego, CA, United States
Elices, Mariano J., San Diego, CA, United States
Zheng, Zhong-Li, Lexington, MA, United States
PA Cytel Corporation, San Diego, CA, United States (U.S. corporation)
PI US 5869448 19990209
AI US 1995-519109 19950825 (8)
RLI Continuation-in-part of Ser. No. US 1995-483077, filed on 7 Jun 1995 which is a continuation-in-part of Ser. No. US 1994-296241, filed on 25 Aug 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Russel, Jeffrey E.
LREP Campbell & Flores LLP
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 2088

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention contemplates a cyclic peptide that inhibits the binding between the VLA-4 receptor expressed on inflammatory leukocytes and the fibronectin CS-1 peptide expressed on endothelial cells that are involved in immunoinflammatory disease states. Pharmaceutical compositions containing a contemplated cyclic peptide and processes for treating immunoinflammatory conditions using a binding-inhibitory cyclic peptide are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 126235-03-8P
(cyclic peptides inhibiting binding of VLA4 receptor and fibronectin CS-1 peptide, compns., and methods of treatment of immunoinflammatory conditions)
IT 107978-77-8
(cyclic peptides inhibiting binding of VLA4 receptor and fibronectin CS-1 peptide, compns., and methods of treatment of immunoinflammatory conditions)

L50 ANSWER 11 OF 13 USPATFULL

AN 1998:115706 USPATFULL
TI Cyclic CS-1 peptidomimetics, compositions and methods of using same
IN Arrhenius, Thomas S., San Diego, CA, United States

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Elices, Mariano J., San Diego, CA, United States
Tempczyk, Anna, San Diego, CA, United States
Zheng, Zhong-Li, Lexington, MA, United States
PA Cytel Corporation, San Diego, CA, United States (U.S. corporation)
PI US 5811391 19980922
AI US 1995-483077 19950607 (8)
RLI Continuation-in-part of Ser. No. US 1994-296241, filed on 25 Aug 1994,
now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Russel, Jeffrey E.
LREP Campbell & Flores LLP
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 1919

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention contemplates a cyclic peptide that inhibits the binding between the VLA-4 receptor expressed on inflammatory leukocytes and the fibronectin CS-1 peptide expressed on endothelial cells that are involved in immunoinflammatory disease states. Pharmaceutical compositions containing a contemplated cyclic peptide and processes for treating immunoinflammatory conditions using a binding-inhibitory cyclic peptide are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 126235-03-8P
(prepn. of cyclic CS-1 peptidomimetics and their compns.)

L50 ANSWER 12 OF 13 USPATFULL

AN 1998:30693 USPATFULL
TI Inhibition of lymphocyte adherence with .alpha.4.beta.1-specific antibodies
IN Wayner, Elizabeth A., St. Paul, MN, United States
PA Fred Hutchinson Cancer Research Center, Seattle, WA, United States (U.S. corporation)
PI US 5730978 19980324
AI US 1994-338282 19941114 (8)
RLI Continuation of Ser. No. US 1991-814873, filed on 24 Dec 1991, now abandoned which is a continuation-in-part of Ser. No. US 1989-402389, filed on 1 Sep 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Feisee, Lila; Assistant Examiner: Gambel, Phillip
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2876

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to a method for inhibiting the adhesion of one cell to another comprising interfering with the interaction between the extracellular matrix receptor and its ligand.

The invention is based upon the discovery that the .alpha.4.beta.1 extracellular matrix receptor promotes adhesion of lymphocytes to endothelial cells via attachment to a defined peptide sequence. Prior to the present invention, the ligand of the .alpha.4.beta.1 receptor had not been identified, nor had the function of the .alpha.4.beta.1 receptor in lymphocyte attachment been known. By preventing the interaction between the .alpha.4.beta.1 receptor and its ligands using antibodies or defined peptide sequences, the present invention enables, for the first time, specific intervention in the migration of

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lymphocytes through the vascular endothelium and into tissues. The present invention, therefore, has particular clinical utility in suppression of the immune response; in various specific embodiments of the invention, the adherence of lymphocytes to endothelium may be inhibited systemically, or may, alternatively, be localized to particular tissues or circumscribed areas. Accordingly, the present invention provides for treatment of diseases involving autoimmune responses as well as other chronic or relapsing activations of the immune system, including allergy, asthma, and chronic inflammatory skin conditions.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 136466-51-8

(binding of, or fragment or homologous sequence of, to .alpha.4.beta.1 extracellular matrix receptor for inhibition of lymphocyte adhesion to endothelial cell)

IT 126235-03-8 128701-34-8

(fibronectin-derived peptide, effect of, on lymphocyte adhesion to endothelial cell, .alpha.4.beta.1 extracellular matrix receptor in relation to)

L50 ANSWER 13 OF 13 USPATFULL

AN 96:34108 USPATFULL

TI Process to inhibit binding of the integrin .alpha..sub.4 62 .sub.1 to VCAM-1 or fibronectin and linear peptides therefor.

IN Kogan, Timothy P., Sugar Land, TX, United States

Ren, Kaijun, Sugar Land, TX, United States

Vanderslice, Peter, Houston, TX, United States

Beck, Pamela J., Houston, TX, United States

PA Texas Biotechnology Corporation, Houston, TX, United States (U.S. corporation)

PI US 5510332 19960423

AI US 1994-271830 19940707 (8)

DT Utility

FS Granted

EXNAM Primary Examiner: Chan, Christina Y.; Assistant Examiner: Prickril, Benet

LREP Dressler, Goldsmith, Shore & Milnamow, Ltd.

CLMN Number of Claims: 15

ECL Exemplary Claim: 1,5

DRWN No Drawings

LN.CNT 1344

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention is directed to an isolated and purified peptide comprising the LDV domain of the CSI peptide sequence or single amino acid substituent analog thereof. A preferred peptide has the amino acid residue sequences shown in SEQ ID NOs:8-14, 17-23, 25, 28, and 51. The present invention is further directed to a process of inhibiting the binding of .alpha..sub.4 .beta..sub.1 integrin to a protein such as VCAM-1 or fibronectin comprising exposing a cell that expresses .alpha..sub.4 .beta..sub.1 integrin to the protein in the presence of an effective inhibiting amount of such a peptide. The present invention is still further directed to a pharmaceutical composition comprising a peptide of SEQ ID NO:8-102.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 159680-18-9DP, conjugates with polyethylene glycol

176955-06-9DP, conjugates with polyethylene glycol

(inhibition of binding of integrin .alpha.4.beta.1 to VCAM-1 or fibronectin with fibronectin CS1 domain peptide analog inhibitors)

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(FILE 'HOME' ENTERED AT 08:01:33 ON 10 JUN 2002)
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FILE 'REGISTRY' ENTERED AT 08:01:43 ON 10 JUN 2002

E EILDV/SQEP
L1 16 S E3
L2 512 S EILDV/SQSP
L3 496 S L2 NOT L1
SAV L1 GAM251073A/A
SAV L3 GAM251073B/A

FILE 'HCAOLD' ENTERED AT 08:02:50 ON 10 JUN 2002

L4 0 S L1 OR L3

FILE 'HCAPLUS' ENTERED AT 08:02:59 ON 10 JUN 2002

L5 20 S L1
L6 351 S L3
L7 9 S EILDV
E LOBB R/AU
L8 113 S E3,E5,E7,E8
E BURKLY L/AU
L9 82 S E3-E6
E BIOGEN/PA,CS
L10 647 S E3-E56
L11 4 S L5-L7 AND L8-L10
L12 363 S L5-L7
L13 2 S L12 AND ?ASTHMA?
E ASTHMA/CT
E E3+ALL
L14 9231 S E2+NT
E E4+ALL
L15 6156 S E6,E5+NT
E E10+ALL
E E5+ALL
L16 8875 S E5,E4+NT
E E11+ALL
E E6+ALL
L17 681 S E4,E3+NT
L18 1 S L12 AND L14-L17
L19 35 S L12 AND (LUNG OR PULMON? OR AIRWAY OR AIR WAY OR BRONCH? OR R
L20 2 S L13,L18
E RESPIR/CT
E E13+ALL
L21 38379 S E5,E4+NT
L22 944 S E36+NT
E E38+ALL
L23 115430 S E4+NT
E E3+AKK
E E3+ALL
E E73+ALL
L24 700 S E2
E RESPIRATORY TRACT/CT
E E42+ALL
L25 177 S E1
E E2+ALL
L26 115430 S E4+NT
L27 18 S L12 AND L21-L26
L28 18 S L27 AND L19
L29 23 S L20,L28,L11
L30 16 S L19 NOT L29
L31 1 S L30 AND RESPIRATORY DISTRESS SYNDROME
L32 24 S L29,L31

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L33 3 S L12 AND HYPERSENSITIV?
L34 3 S L12 AND ?ALLERG?
L35 5 S L33,L34
L36 1 S L35 AND L32
L37 4 S L35 NOT L32
L38 24 S L32,L36
L39 5 S L38 AND (PY<=1993 OR PRY<=1993 OR AY<=1993)
L40 1 S L39 AND L13,L18
L41 19 S L38 NOT L39
SEL DN 18
L42 1 S E1 AND L41
L43 2 S L40,L42
L44 4 S L11,L20 NOT L43
SEL HIT RN L43

FILE 'REGISTRY' ENTERED AT 08:23:14 ON 10 JUN 2002

L45 9 S E2-E10
L46 9 S L45 AND L1-L3

FILE 'USPATFULL, USPAT2' ENTERED AT 08:23:49 ON 10 JUN 2002

L47 53 S L1,L3
L48 13 S L47 AND ?ASTHMA?
L49 1 S L47 AND (ASTHMA? OR ANTI-ASTHMA?)/CT
L50 13 S L48,L49
L51 0 S L50 AND (PY<=1993 OR PRY<=1993)
L52 4 S L47 AND (PY<=1993 OR PRY<=1993)
L53 27 S L47 AND (BRONCH? OR LUNG? OR PULMONARY? OR RESPIRATION? OR RE
L54 0 S L52 AND L53

FILE 'HCAPLUS' ENTERED AT 08:26:10 ON 10 JUN 2002

FILE 'REGISTRY' ENTERED AT 08:26:18 ON 10 JUN 2002

FILE 'HCAPLUS' ENTERED AT 08:26:38 ON 10 JUN 2002
SEL HIT RN L44

FILE 'REGISTRY' ENTERED AT 08:27:17 ON 10 JUN 2002

L55 6 S E11-E16
L56 4 S L55 AND L1-L3 NOT L46

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